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GM protein - protein search, using sw model

Run on: June 22, 1999, 10:59:47 ; Search time 45.16 Seconds

(without alignments)
93,311 Million cell updates/sec

Title: US-09-030-061-7

RefSeq source: 812

Sequence: 1 NESHRTTAVRININDVL

Scoring table: BLISSUMC2

Database: SwissProt_36*

Fried, No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No	Score	Query Match Length	DB ID	Description
1	812	100	1	IL18_MOUSE
2	742.5	91.4	1	IL18_PAT
3	520	193	1	IL18_HUMAN
4	362	160	1	IL18_PIG
5	83.5	10.3	1	IL18_HAVIN
6	81	10.0	1	IL18_PIG
7	80.5	9.5	1	IL18_PIG
8	80	9.4	1	IL18_PIG
9	79.5	9.4	1	IL18_PIG
10	79	9.7	1	IL18_PIG
11	78.5	9.7	1	IL18_PIG
12	78.5	9.7	1	IL18_PIG
13	77.5	9.5	1	IL18_PIG
14	77.5	9.5	1	IL18_PIG
15	76.5	9.4	1	IL18_PIG
16	76.5	9.4	1	IL18_PIG
17	75	9.2	1	IL18_PIG
18	75	9.2	1	IL18_PIG
19	75	9.2	1	IL18_PIG
20	74.5	9.2	1	IL18_PIG
21	74	9.1	1	IL18_PIG
22	74	9.1	1	IL18_PIG
23	74	9.1	1	IL18_PIG
24	74	9.1	1	IL18_PIG
25	74	9.1	1	IL18_PIG
26	74	9.1	1	IL18_PIG
27	73	9.0	1	IL18_PIG
28	72.5	8.9	1	IL18_PIG
29	72.5	8.9	1	IL18_PIG
30	72	8.9	1	IL18_PIG
31	72	8.9	1	IL18_PIG
32	71.5	8.7	1	IL18_PIG
33	71.5	8.7	1	IL18_PIG
34	71	8.7	1	IL18_PIG
35	71	8.7	1	IL18_PIG
36	71	8.7	1	IL18_PIG
37	71	8.7	1	IL18_PIG
38	70.5	8.7	1	IL18_PIG
39	70.5	8.7	1	IL18_PIG
40	70.5	8.7	1	IL18_PIG
41	70.5	8.7	1	IL18_PIG
42	70.5	8.7	1	IL18_PIG
43	70	8.6	1	IL18_PIG

ALIGNMENTS

44 70 8 6 1613 1 VIL12_CAFEL
45 70 8 6 1613 1 VIL12_CAFEL

RESULT 1
IL18_MOUSE
AC P70380
DT 15-JUL-1998 (REL. 36, CREATED)
DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE INTERLEUKIN-18 PREPROPEP (11-18) (INTERFERON-GAMMA INDUCING FACTOR)
DE (IFN-GAMMA-INDUCING FACTOR) (INTERLEUKIN-1 GAMMA) (IL-1 GAMMA).
OS MMS MURICUS (MURUS).
GN IL18 OR IGIF.
OC EUTHERIA: MAMMALIA: VERTEBRATA: MAMMALIA: VERTEBRATA: MAMMALIA: VERTEBRATA: RODENTIA: (11)
RN SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
PP TISSUE-LIVER.
PC MEDLINE: 96061009.
RA OKAMURA H., ISHII H., KOMATSU T., YUTSUKO M., HAKURA A.,
RA TANIMOTO T., TERASHIMA Y., OKURA T., NITADA Y., HATSUBI K.,
RA AKITA K., NAKABA M., TANABE F., KONISHI K., FUKUDA S., KURIMOTO M.:
NATURE 378:88-91(1995).
SN (12)
RP SEQUENCE OF 1-191 FROM N.A.
RC STRAIN-NOD: TISSUE-PANCREAS:
RX MEDLINE: 97174346.
RA BOTHER H., JENKINS N.A., COFFLAND N.G., KOUB H.:
RA J. CLIN. INVEST. 94:463-474(1997).
CC AN. STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE 1
CELLS.
CC EMBL: 140444; GI: 444938.
DR EMBL: 066444; S15017355.
DR MIM: MIM:107846; IGIF.
KW CYTOKINE.
FT PROPEP 1 35 INTERLEUKIN-18.
FT CHAIN 36 192 MFT 35 IS (IN REF. 2).
FT SIGNAL 192 195
SQ SEQUENCE 192 AA; 28136 MB; 46320875 DECIBIT.

Query Match 100 0% Score 812; DB 1; Length 192;
Host Local Similarity 100.0%; E-Val 2.1e-65;
Matches 157; Conserved 0; Mismatches 0; Indels 0; Gaps

1 NESHRTTAVRININDVLVFKRPVFLKMTIRNSASR...
2 NESHRTTAVRININDVLVFKRPVFLKMTIRNSASR...
3 NESHRTTAVRININDVLVFKRPVFLKMTIRNSASR...
4 NESHRTTAVRININDVLVFKRPVFLKMTIRNSASR...
5 NESHRTTAVRININDVLVFKRPVFLKMTIRNSASR...
6 NESHRTTAVRININDVLVFKRPVFLKMTIRNSASR...
7 NESHRTTAVRININDVLVFKRPVFLKMTIRNSASR...
8 NESHRTTAVRININDVLVFKRPVFLKMTIRNSASR...
9 NESHRTTAVRININDVLVFKRPVFLKMTIRNSASR...
10 NESHRTTAVRININDVLVFKRPVFLKMTIRNSASR...
11 NESHRTTAVRININDVLVFKRPVFLKMTIRNSASR...
12 NESHRTTAVRININDVLVFKRPVFLKMTIRNSASR...
13 NESHRTTAVRININDVLVFKRPVFLKMTIRNSASR...
14 NESHRTTAVRININDVLVFKRPVFLKMTIRNSASR...
15 NESHRTTAVRININDVLVFKRPVFLKMTIRNSASR...
16 NESHRTTAVRININDVLVFKRPVFLKMTIRNSASR...
17 NESHRTTAVRININDVLVFKRPVFLKMTIRNSASR...
18 NESHRTTAVRININDVLVFKRPVFLKMTIRNSASR...
19 NESHRTTAVRININDVLVFKRPVFLKMTIRNSASR...
20 NESHRTTAVRININDVLVFKRPVFLKMTIRNSASR...
21 NESHRTTAVRININDVLVFKRPVFLKMTIRNSASR...
22 NESHRTTAVRININDVLVFKRPVFLKMTIRNSASR...
23 NESHRTTAVRININDVLVFKRPVFLKMTIRNSASR...
24 NESHRTTAVRININDVLVFKRPVFLKMTIRNSASR...
25 NESHRTTAVRININDVLVFKRPVFLKMTIRNSASR...
26 NESHRTTAVRININDVLVFKRPVFLKMTIRNSASR...
27 NESHRTTAVRININDVLVFKRPVFLKMTIRNSASR...
28 NESHRTTAVRININDVLVFKRPVFLKMTIRNSASR...
29 NESHRTTAVRININDVLVFKRPVFLKMTIRNSASR...
30 NESHRTTAVRININDVLVFKRPVFLKMTIRNSASR...
31 NESHRTTAVRININDVLVFKRPVFLKMTIRNSASR...
32 NESHRTTAVRININDVLVFKRPVFLKMTIRNSASR...
33 NESHRTTAVRININDVLVFKRPVFLKMTIRNSASR...
34 NESHRTTAVRININDVLVFKRPVFLKMTIRNSASR...
35 NESHRTTAVRININDVLVFKRPVFLKMTIRNSASR...
36 NESHRTTAVRININDVLVFKRPVFLKMTIRNSASR...
37 NESHRTTAVRININDVLVFKRPVFLKMTIRNSASR...
38 NESHRTTAVRININDVLVFKRPVFLKMTIRNSASR...
39 NESHRTTAVRININDVLVFKRPVFLKMTIRNSASR...
40 NESHRTTAVRININDVLVFKRPVFLKMTIRNSASR...
41 NESHRTTAVRININDVLVFKRPVFLKMTIRNSASR...
42 NESHRTTAVRININDVLVFKRPVFLKMTIRNSASR...
43 NESHRTTAVRININDVLVFKRPVFLKMTIRNSASR...

RESULT 2
IL18_PAT
AC P97636; P97637;
DT 15-JUL-1998 (REL. 36, CREATED)
DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
DE INTERLEUKIN-18 PREPROPEP (11-18) (INTERFERON-GAMMA INDUCING FACTOR)
DE (IFN-GAMMA-INDUCING FACTOR) (INTERLEUKIN-1 GAMMA) (IL-1 GAMMA).
OS MMS MURICUS (MURUS).
GN IL18 OR IGIF.
OC EUTHERIA: MAMMALIA: VERTEBRATA: MAMMALIA: VERTEBRATA: RODENTIA: (11)
RN SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
PP TISSUE-LIVER.
PC MEDLINE: 96061009.
RA OKAMURA H., ISHII H., KOMATSU T., YUTSUKO M., HAKURA A.,
RA TANIMOTO T., TERASHIMA Y., OKURA T., NITADA Y., HATSUBI K.,
RA AKITA K., NAKABA M., TANABE F., KONISHI K., FUKUDA S., KURIMOTO M.:
NATURE 378:88-91(1995).
SN (12)
RP SEQUENCE OF 1-191 FROM N.A.
RC STRAIN-NOD: TISSUE-PANCREAS:
RX MEDLINE: 97174346.
RA BOTHER H., JENKINS N.A., COFFLAND N.G., KOUB H.:
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CC AN. STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE 1
CELLS.
CC EMBL: 140444; GI: 444938.
DR EMBL: 066444; S15017355.
DR MIM: MIM:107846; IGIF.
KW CYTOKINE.
FT PROPEP 1 35 INTERLEUKIN-18.
FT CHAIN 36 192 MFT 35 IS (IN REF. 2).
FT SIGNAL 192 195
SQ SEQUENCE 192 AA; 28136 MB; 46320875 DECIBIT.

01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE APP-DEPENDENT PROTEINASE LA (EC 3.4.21.53)
 GN LON OR LON A OR H10462.
 OS HAEMOPHILUS INFLUENZAE
 CC PROKARYOTIC, GRACILICUTES, NON-CHARACTERIAL, FACULTATIVELY ANAEROBIC BODIES,
 CC PASTEURILLACEAE.
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-RT, RW3
 RC MEDLINE: 9637930
 RA FLEISCHMANN R D, ADAMS M D, WHITE C, CLAYTON P A, KIRKNESS E F,
 RA KERVINAGE A F, RITT J J, TOME T F, EDGHEEY P A, MERRICK J M,
 RA MCKENNEY R, STATION G, FITZBUSH W A, JOOYAVE J D,
 RA SCOTT J D, SHIPLEY F, JIN L T, STODER A, KELLEY T M,
 RA STRIMAN T F, PHILLIPS C A, SARRIGOS T, HERBOW E, COTTON M D,
 RA DUTERBACK T R, HANNA M C, NGUYEN D T, SANDER D M, BRANTON R C,
 RA FINE I D, FRITZMAN J L, FUHRMAN J L, GEOGHAGAN N S M,
 RA GHEM C J, McDONALD L A, SMALL K V, FRASER C M, SMITH H O,
 RA VENTER J C,
 RL SCIENCE 266:496-512(1995).
 CC -1- FUNCTION: DEGRADATES SHORT-LIVED REGULATORY AND ANIONIC PROTEINS
 CC IN PRESENCE OF ATP DEGRADATES THE REGULATORY PROTEINS P2A AND
 CC S2A. HYDROLYSES TWO ATPs FOR EACH PEPTIDE BOND CLEAVED IN THE
 CC PROTEIN SUBSTRATE (BY SIMILARITY).
 CC -2- CATALYTIC ACTIVITY: HYDROLYSIS OF LARGE PROTEINS SUCH AS GLOBIN,
 CC CASEIN AND DEGRADATES SERUM ALBUMIN, IN PRESENCE OF ATP
 CC -3- SPECIFIC AMOXYLAMER (BY SIMILARITY)
 CC -4- SPECIFIC LOCATION: CYTOSOL
 CC -5- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S16; ALSO KNOWN AS THE
 CC CON FAMILY OF ATP-DEPENDENT PROTEASES.
 DR EMBL: U22720 (C1573410)
 DR TIGR: H10462
 DR PROSITE PROSITE: ION SEPT. 1
 KN HYDROLASE: SERINE PROTEASE: ATP-BINDING.
 FT NE-BIND 368
 FT ACT-SITE 679
 FT 679
 SO SEQUENCE: 679 AA 8347 MW 1464896.057102

Query Match 10.84, Score 83.5, DB 1, Length 803.
 Best local similarity 10.94, Proj No 4.4;
 Matches 44; Conservative 33; Mismatches 71; Indels 85; Gaps 7;

0Y 3 GRACILICUTES-DEVELOPER-OPVEDMIDIDOSAS-41
 DB 30 GRACILICUTES-DEVELOPER-OPVEDMIDIDOSAS-41
 0Y 41 -EPOXIDOLIPID-VEGIATILSYKSKMSLSTKNNISFE 83
 DB 30 VECONDAKILSTFEKTESAQTITTEYREKEIVAKSAVSEFENYLTINKKVPID 149
 0Y 34 EMPRENTID-OSLIDIFOK 103
 DB 100 TIRAFITV RITAFARFVSTFRRNMI ELANVAPFETLLMKSEALDVERK 209
 0Y 104 RYGHNMKEFESSLYEGH LADYKELHAKILKKLENGDKSVMTLHNO 156
 DB 210 RYGHNMKEFESSLYEGH LADYKELHAKILKKLENGDKSVMTLHNO 156

RESULT 5
 ID ILIB-PIG STANDARD PPT 267 AA
 AC 102837
 DI 01-AUG-1992 (REL. 23, CREALED)
 DI 01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
 DI 01-NOV-1994 (REL. 32, LAST ANNOTATION UPDATE)
 DI INTERFERIN-1 BETA PRECURSOR (IL-1 BETA)
 GN IL1B
 OS SUS SCROFA (PIT)
 CC EUKARYOTA METAZOA CHORDATA VERTEBRATA TETRAPODA MAMMALIA
 CC BIRHETIA ARTIODACTYLA
 RN (1)

RP SEQUENCE FROM N.A.
 RX MEDLINE: 9331975
 RA HORTER M O, LIN S, SMITH D M, MURTAGH M E, MILLER T W,
 RC GENE 109:299-299(1993)
 CC -1- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
 CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
 CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
 CC IL-1 PROTEIN ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
 CC IDENTIFIED AS IMMUNOGENS, PYROGEN, AND ARE REPORTED TO STIMULATE
 CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
 CC -2- STRUTIN: MONOMER.
 CC -3- THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE AMINO
 CC ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
 CC -4- THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE PRECURSOR
 CC SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY TAMARCT CELLS OR IS
 CC SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
 CC SECRETORY PROTEINS.
 CC -5- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
 DR EMBL: M6725; G164608;
 DR PIP: J08724; J08724.
 DR HSP: P01584; I1B1.
 DR PROSITE: P00053; INTERLEUKIN-1;
 KW CYTOKINE; MACROPHAGE; MILK; INFLAMMATORY RESPONSE; PYROGEN.
 FT PROPEP 114
 FT CHAIN 115 267
 FT CAPRHVD 46 46
 FT CAPRHVD 59 59
 FT CAPRHVD 59 59
 SO SEQUENCE: 267 AA: 30404 MW: 59300FAB C0022;

Query Match 10.04, Score 81, DB 1, Length 267;
 Best local similarity 26.14, Proj No 2;
 Matches 27; Conservative 22; Mismatches 21; Indels 12; Gaps 5;

0Y 49 YMKSEVGLAVLSYKSKMSLSTKNNISFEK-PEPIDOSLIDIF 101
 DB 100 YMKSEVGLAVLSYKSKMSLSTKNNISFEK-PEPIDOSLIDIF 101
 0Y 102 OKRPOHNMKEFESSLYEGH LADYKELHAKILKKLENGDKSVMTLHNO 156
 DB 217 PTEI-FNVEFESLIPMWISTEQAE 242

RESULT 7
 ID ZABA-YEAST STANDARD PPT 526 AA
 AC 000362;
 DI 01-APR-1993 (REL. 25, CREATED)
 DI 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 DI 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DI PROTEIN PHOSPHATASE P2A REGULATORY SUBUNIT B (P25) (CELL DIVISION
 DE CONTROL PROTEIN 55)
 GN CONTROL OF YEAST OR G1345.
 OS SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 CC EUKARYOTA FUNGI ASCOMYCOTINA HEMIASCOMYCETES.
 RN (1)
 RP SEQUENCE FROM N.A.
 RC MEDLINE: 9637930
 RA HEALY A M, ZONIEROWICZ S, STAPLETON A E, GOEBL M,
 RA DEPAULI-ROACH A A, PRINGLE J P,
 RL MOL. CELL. BIOL. 11:5767-5780(1991).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC MEDLINE: 9719771
 RA COCHRAN X, FRYM S, BEHANT I, DIERRE E, ZACARIA P,
 RA YEASU 13:55-64(1997).
 CC -1- FUNCTION: PHOSPHATASE 2A AFFECTS A VARIETY OF BIOLOGICAL PROCESSES
 CC IN THE CELL SUCH AS TRANSCRIPTION, CELL CYCLE PROGRESSION AND
 CC CELLULAR MORPHOGENESIS, AND PROVIDES AN INITIAL IDENTIFICATION OF
 CC CRITICAL SUBSTRATES FOR THIS PHOSPHATASE THE PROTEIN KINASE SUBUNIT
 CC MAY DIRECT THE CATALYTIC SUBUNIT TO DISTINCT ALLELIC OVERLAPPING.

SEQUENCE FROM N.A.
 RA MEDLINE: 86318632.
 RA MALLICKSRI Q. R. PAKER E. E. STEINBERG M. A. TAVIS R. S. GOSMAN D.
 RA GILLIS S. J. CERRETTI D. P. J.
 RA MOLL. IMMUNOL. 25:426-437(1988).
 CC 1 FUNCTION: PROCEDED BY ACTIVATED MACROPHAGES. IL-1 STIMULATES
 CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE. B-CELL
 CC MATURATION & PROLIFERATION. & FIBROBLAST GROWTH FACTOR ACTIVITY
 CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
 CC IDENTIFIED AS ENDOTOXINS PYROGEN, AND ARE REPORTED TO STIMULATE
 CC THE RELEASE OF PRO-INFLAMMIN AND COLLAGENASE FROM SYNOVIAL CELLS.
 CC SUBUNIT: MONOMER.
 CC -1- THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE AMINO
 CC ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
 CC -1- THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE PRECURSOR
 CC SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS OR IS
 CC SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
 CC SECRETORY PROTEINS.
 CC -1- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
 DR EMBL: X12498: G4493-1.
 DR EMBL: M9221: G16201-1.
 DR PIR: J10010: 10010.
 DR F1R: S01560: S01560.
 DR HSSP: P01584: 1H1F.
 DR PROSITE: PS00253: INTERLEUKIN_1.
 DR CYTOKINE: ESD0253: INTERLEUKIN_1.
 KW CYTOKINE. MATRPHAC. MITOGEN. INFLAMMATORY RESPONSE. PYROGEN.
 FT PROPEP 1 113
 FT CHAIN 114 256 INTERLEUKIN-1 BETA.
 FT CARBOHYD 58 58 POTENTIAL
 FT CONFLICT 252 252 A-252 (IN PEP. 2).
 FT SEQUENCE 156 AA 30774 MW: 10627850 GRC32

Query Match 9.7% Score 79; DB 1; Length 266;

Best Local Similarity 26.7% Pctd. No. 3;
 Matches 32; Conservative 19; Mismatches 31; Indels 36; Gaps 8;

QY 40 SEQPTLLIYKDEVR-----LAVLSYKSKMSTLCKK-----IISPEMP-- 88
 DB 148 SFPMRFFVGR-SFVGRERKNIYAGIKKNL-YLSYKKSITFLQLEVEYKV 202
 QY 88 -PENIDIOSLIFQKPYGKMKPESSLYE-----GHFLACQEDD 130
 DB 203 YKRS--NMKEHYVYKIEL--KNIVEPSVLYPMWYISTSIEPRVPLGFRAGQDITD 258

RESULT 11
 ID IL1A_MOUSE STANDARD: PRT: 270 AA
 AC P01582;
 DT 01-NOV-1984 (REL. 40, LAST SEQUENCE UPDATE)
 DT 01-NOV-1984 (REL. 40, LAST SEQUENCE UPDATE)
 DT 01-NOV-1984 (REL. 34, LAST ANNOTATION UPDATE)
 DE INTERLEUKIN-1 ALPHA PRECURSOR (H1A1 ALPHA)
 GN IL1A.
 OS MUS MUSCULUS (MOUSE).
 CC STRAINTA METAC72. H. FRATA. VFFTFPATA. TTFAPODA. MAMMALIA.
 CC EUTHERIA. PENTIA.
 RN 11;
 RP SEQUENCE FROM N.A.
 RA MEDLINE: 85061582.
 RA LONEDING P. T. GRIFFIN P. HELLMANN C. P. DUKOVICH M. G. G. P. I. G.
 RA PAN Y. C. E. COLLIER K. SEMINOW F. CHUA A. G. MIZEL S. B.
 RA NATURE 312:458-462(1984)
 RN 12;
 RP SEQUENCE FROM N.A.
 RA MEDLINE: 89153709.
 RA RENSCHER H. H. NICKELLS M. W. COTTEN H. P.
 RA J. BIOL. CHEM. 263:4023-4028(1988).
 CC -1- FUNCTION: PROCEDED BY ACTIVATED MACROPHAGES. IL-1 STIMULATES
 CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE. B-CELL
 CC MATURATION & PROLIFERATION. & FIBROBLAST GROWTH FACTOR ACTIVITY

IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
 IDENTIFIED AS ENDOTOXINS PYROGEN, AND ARE REPORTED TO STIMULATE
 THE RELEASE OF PRO-INFLAMMIN AND COLLAGENASE FROM SYNOVIAL CELLS.
 SUBUNIT: MONOMER.
 -1- THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE AMINO
 ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
 -1- THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE PRECURSOR
 SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS OR IS
 SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
 SECRETORY PROTEINS.
 -1- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
 DR EMBL: X01450: G52669-1.
 DR PIR: A01845: 10MS1.
 DR HSSP: P01583: 1H1A.
 DR M6D: M6196342: 1H1A.
 DR PROSITE: PS00253: INTERLEUKIN_1.
 DR CYTOKINE: ESD0253: INTERLEUKIN_1.
 KW CYTOKINE. MATRPHAC. MITOGEN. INFLAMMATORY RESPONSE. PYROGEN.
 FT PROPEP 1 114
 FT CHAIN 115 270 INTERLEUKIN-1 ALPHA.
 FT MODRES 90 90 PHOSPHORYLATION.
 FT CARBOHYD 54 54 POTENTIAL.
 FT CONFLICT 139 139 POTENTIAL.
 FT SEQUENCE 143 143
 DB 243 PEPFLATKED 252

Query Match 9.7% Score 78.5; DB 1; Length 270;

Best Local Similarity 23.8% Pctd. No. 3.4;
 Matches 31; Conservative 28; Mismatches 40; Indels 31; Gaps 7;

QY 15 YKRS--NMKEHYVYKIEL--KNIVEPSVLYPMWYISTSIEPRVPLGFRAGQDITD 164
 DB 138 MMSD-----MOTIVLQVKNYSTLWNLQ-----EVEFMVYSSGLSK--YF 164
 QY 119 FGFPLATKED 138
 DB 185 VLKISDGLSVSAGCEQVPLKELPEIKLISGELLFFWKT--NKNVYFSAAY 242

RESULT 12
 ID YB06_YEAST STANDARD: PRT: 698 AA.
 AC P38283;
 DT 01-NOV-1984 (REL. 40, CREATED)
 DT 01-NOV-1984 (REL. 40, LAST SEQUENCE UPDATE)
 DT 01-NOV-1984 (REL. 35, LAST ANNOTATION UPDATE)
 DE HYP-CHETICAL 79.2 Kt. Protein in Ref. 2002 INTERLEUKIN-1 REGION.
 GN YB06_YEAST (YB06_YEAST)
 OS SACHAROMYCES CEREVISIAE (BAKER'S YEAST).
 CC EUTHERIA. PENTIA. ANOMYOTINA. HEMIASCOMYCETES.
 RN 11;
 RP SEQUENCE FROM N.A.
 RA NITAN K. D. KOTTER P. POSE M. BEKKER J. GREY V. 11 2.
 RA NIESEMAN E. SCHENK-GROENINGER R. SEVOS. WEHNER E.
 RA WILTER P. ROENIGT M. RAUER J. RAU H. G. K. N. P. N. S. S.
 RA GRENDELIN F. HELGES D. KIESAU P. KOBOL S. KREMS B. FROST M.
 RA STREPE K. BAUR A. BOLES E. MIOGA T.
 RA SCHWAB-DEPENSCHLAEDER T. ZIMMERMANN F. K.
 RA SCHWAB (1984) TO EMBL/GENBANK/DBT DATA BANKS
 RN 12;
 RP SEQUENCE FROM N.A.
 RA STRAIN-S288C;
 RA MEDLINE: 93255907.
 RA PATE A. J. SCHWAB-DEPENSCHLAEDER T. ZIMMERMANN F. K.
 RA ZIMMERMANN F. K.
 RA YEAST 9:289-293(1993).
 DR EMBL: Z50253: G550458-1;

[illegible]

Search completed. Time 22: 1999, 10:59.48
Job time: 74 sec



GenBank version 4.5
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ON PROTEIN: PROTEIN SEARCH using SW model

File: 09-030-061-1 Search time: 93.17 seconds
(without alignments)
3 980 Million cell updates/sec

Header:
Perfect score
Sequence
Scoring table

Header:
Perfect score
Sequence
Scoring table

Search: 100763 seqs, 55169189 residues

Database:

SPRMBL_8.*
1: sp_fungi.*
2: sp_human.*
3: sp_invertebrate.*
4: sp_mammal.*
5: sp_mhc.*
6: sp_orangutan.*
7: sp_phage.*
8: sp_plant.*
9: sp_prokaryote.*
10: sp_rodent.*
11: sp_virus.*
12: sp_vertebrate.*
13: sp_unclassified.*
14: sp_archaea.*

Result No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	FR	ID	Description
1	31	100.0	194	2	075599	075599 homo sapien
2	31	100.0	194	1	098749	098749 rat/rus mtr
3	28	90.3	782	9	P75808	P75808 eschschilia
4	28	90.3	110	11	057332	057332 vacuola vi
5	28	90.3	117	11	056217	056217 camelpox vi
6	28	90.3	110	11	056272	056272 cowpox vir
7	28	90.3	110	11	083542	083542 mousepox vi
8	28	90.3	110	11	090188	090188 monkeypox v
9	28	90.3	548	14	058508	058508 methanococ
10	28	87.1	126	3	001641	001641 drosophila
11	28	87.1	426	3	062531	062531 drosophila
12	28	87.1	42	3	025522	025522 manduca sex
13	28	87.1	395	3	025495	025495 manduca sex
14	28	87.1	426	3	002382	002382 caenorhabd
15	28	87.1	1763	3	017901	017901 caenorhabd
16	28	87.1	1763	3	017901	017901 caenorhabd
17	28	87.1	1763	3	017901	017901 caenorhabd
18	28	87.1	1763	3	017901	017901 caenorhabd
19	28	87.1	1763	3	017901	017901 caenorhabd
20	28	87.1	1763	3	017901	017901 caenorhabd
21	28	87.1	1763	3	017901	017901 caenorhabd
22	28	87.1	1763	3	017901	017901 caenorhabd
23	28	87.1	1763	3	017901	017901 caenorhabd
24	28	87.1	1763	3	017901	017901 caenorhabd
25	28	87.1	1763	3	017901	017901 caenorhabd
26	28	87.1	1763	3	017901	017901 caenorhabd
27	28	87.1	1763	3	017901	017901 caenorhabd
28	28	87.1	1763	3	017901	017901 caenorhabd
29	28	87.1	1763	3	017901	017901 caenorhabd
30	28	87.1	1763	3	017901	017901 caenorhabd

ALIGNMENTS

RESULT	ID	Query Match	Similarity	Score	DB	Length	FR	ID	Description
1	075599	100.0	100.0	31	DB 2	194	2	075599	075599 homo sapien
2	098749	100.0	100.0	31	DB 2	194	1	098749	098749 rat/rus mtr
3	P75808	90.3	90.3	782	9	P75808	9	P75808	P75808 eschschilia
4	057332	90.3	90.3	110	11	057332	11	057332	057332 vacuola vi
5	056217	90.3	90.3	117	11	056217	11	056217	056217 camelpox vi
6	056272	90.3	90.3	110	11	056272	11	056272	056272 cowpox vir
7	083542	90.3	90.3	110	11	083542	11	083542	083542 mousepox vi
8	090188	90.3	90.3	110	11	090188	11	090188	090188 monkeypox v
9	058508	90.3	90.3	548	14	058508	14	058508	058508 methanococ
10	001641	87.1	87.1	126	3	001641	3	001641	001641 drosophila
11	062531	87.1	87.1	426	3	062531	3	062531	062531 drosophila
12	025522	87.1	87.1	42	3	025522	3	025522	025522 manduca sex
13	025495	87.1	87.1	395	3	025495	3	025495	025495 manduca sex
14	002382	87.1	87.1	426	3	002382	3	002382	002382 caenorhabd
15	017901	87.1	87.1	1763	3	017901	3	017901	017901 caenorhabd
16	017901	87.1	87.1	1763	3	017901	3	017901	017901 caenorhabd
17	017901	87.1	87.1	1763	3	017901	3	017901	017901 caenorhabd
18	017901	87.1	87.1	1763	3	017901	3	017901	017901 caenorhabd
19	017901	87.1	87.1	1763	3	017901	3	017901	017901 caenorhabd
20	017901	87.1	87.1	1763	3	017901	3	017901	017901 caenorhabd
21	017901	87.1	87.1	1763	3	017901	3	017901	017901 caenorhabd
22	017901	87.1	87.1	1763	3	017901	3	017901	017901 caenorhabd
23	017901	87.1	87.1	1763	3	017901	3	017901	017901 caenorhabd
24	017901	87.1	87.1	1763	3	017901	3	017901	017901 caenorhabd
25	017901	87.1	87.1	1763	3	017901	3	017901	017901 caenorhabd
26	017901	87.1	87.1	1763	3	017901	3	017901	017901 caenorhabd
27	017901	87.1	87.1	1763	3	017901	3	017901	017901 caenorhabd
28	017901	87.1	87.1	1763	3	017901	3	017901	017901 caenorhabd
29	017901	87.1	87.1	1763	3	017901	3	017901	017901 caenorhabd
30	017901	87.1	87.1	1763	3	017901	3	017901	017901 caenorhabd


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RN      [1]
RP      SEQUENCE FROM N.A.
EX      MERLIN; 97067009
CY      JIANG H., WANG Y., HEWANG Y., MULNIX A.B., KADFI J., MOLE K.,
        KANDSI M.P.;
RT      "Organization of serpin gene1 from Manduca sexta. Evolution of a
RL      family of alternate exons encoding the reactive site loop."
RE      J. Biol. Chem. 271:8017-8022(1996).
DR      EMBL: U058361; G1378131;
PR      PF00079; Serpin1.1;
SC      209 AA; 1741 MW; 250562 DCD22;

Query Match          87.1%; Score 27; DB 3; Length 209;
Best Local Similarity 83.3%; Pred. No. 84;
Matches    5; Conservative   0; Mismatches     0; Indels    0; Gaps    0;

CY      1 NDQVLF 6
         ||| ||
DB      383 NDQVLF 388

RESULT  14
ID      Q02282              PRELIMINARY             FRT: 425 AA.
AC      Q02282
DT      01-JUL-1997 (TRERMLREL 04; CREATED)
DI      01-JUL-1997 (TRERMLREL 04; LAST SEQUENCE UPDATE)
LI      01-NOV-1998 (TRERMLREL 08; LAST ANNOTATION UPDATE)
DE      KLND2.3
OS      CAUCHORHABDITIS ELEGANS.
OC      PHARIPTIDA; MELENYON; NEMATODA; SPIROBRANCHIA; PHARIPTIDAE; PHARIPTINAE;
OC      PHARIPTIDAE; PHARIPTIDAE; PHARIPTIDAE; PHARIPTIDAE; PHARIPTIDAE;
CC      [1];
PP      SEQUENCE FROM N.A.
RA      KERSHAW J.;
RC      SCHMITTER L.W. 1996; 1 EYE; PNEUMATICALLY INACT. ORNS.
KN      [2].
RP      SEQUENCE FROM N.A.
RX      MEDLINE; 94150718.
RA      WINSON S., ALINGBACH F., ANDERSEN B., FAIRMAN J., ERIC M., HENRIEL J.,
RA      BOUTON I., CONNELLY M., CORSEY T., COOPER J., CUSAN A., DEANIN M.,
RA      BEER S., DE ZEELEN B., FAVELL A., FOJON V., GARNIER A., GREEN P.,
RA      HARVEY R., HILLIER S., JIEEM M., JOHNSON J., JES M., KASPARAK J.,
RA      KRISTEN J., LAISTER N., LATRILLE P., LIGHTNING J., LILOYD C.,
RA      MCMPRAY A., MORTIMORE B., O'CALLAGHAN M., PAWS NS J., PERCY C.,
RA      PIVERE E., POCHFA A., SANDERS F., SHANKSKEIN F., SMITH N.N., SMITH A.,
RA      SONNHAMMER E., STADEN P., SULSTON J., THIERRY-MIEG J., THOMAS R.,
RA      VALETTE M., VASCHAN R., WATERSON F., WALSTEIN A., WEINSACK L.,
RA      WILKINSON-SPOUT J., WORLDMAN P.;
RT      "2.2 Mb of chromosome band 10A contains the sequence from chromosome III of C.
RT      elegans."
RL      NATURE 368:32-38(1994);
RE      EMBL: Z81151; E315237;
PR      PF00928; Adap_comp_subj: 1;
SC      SEQUENCE 425 AA; 49841 MW; 250562 DCD22;

Query Match          87.1%; Score 27; DB 3; Length 425;
Best Local Similarity 83.3%; Pred. No. 90;
Matches    5; Conservative   1; Mismatches     0; Indels    0; Gaps    0;

CY      1 NDQVLF 6
         ||| ||
DB      209 NDQVLF 214

RESULT  15
ID      Q17901              PRELIMINARY             FRT: 1763 AA.
AC      Q17901
DT      01-NOV-1996 (TRERMLREL 01; CREATED)
DI      01-NOV-1996 (TRERMLREL 08; LAST SEQUENCE UPDATE)
LI      01-NOV-1996 (TRERMLREL 08; LAST SEQUENCE UPDATE)

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DT 01-NOV-1998 (HEMELBEL, 08, LAST ANNOTATION UPDATE)
 DE C10C5.6 PROTEIN.
 GN C10C5.6
 OS CAENORHABDITIS ELEGANS.
 OC ELMARINIA, NEMATODA, SECERNENTEA, RHABDITIA, RHABDITIDA;
 OC RHABDITINA, RHABDITIDAE, RHABDITINAE, PTEROPHARINAE, CAENORHABDITIS.
 RN 111
 RP SEQUENCE FROM N.A.
 RA MATTHEWS F.
 RL SUBMITTED (NOV-1995) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN 121
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 94150718.
 RA WILSON P., AINSCOUGH P., ANDERSON K., BAYNES C., BERKS M., BONFIELD J.,
 RA BERTON T., CONNELL M., GOSSEY I., GUMPER J., JOHNSON A., GRAXTON M.,
 RA DEAR S., DRYZ, EMERIN P., FAVELLO A., FULTON L., GARDNER A., GREEN P.,
 RA HAWKINS T., HILLIER T., JEFF M., JOHNSTON L., JONES M., KERSHAW J.,
 RA KRISTEN T., LAISTER N., LATREILLE P., LIGHTNING J., LLOYD C.,
 RA MCMURRAY A., MORTIMORE B., O'CALLAGHAN M., PARSONS J., PERCY C.,
 RA RIFKIN L., POPPRA A., SAUNDERS D., SHOWNKEEN R., SMALDON N., SMITH A.,
 RA SONNHAUER E., STADEN P., STILSTON J., THIERRY-MIEG J., THOMAS K.,
 RA VAUGHAN M., VANGHAN K., WATERSTON P., WATSON A., WEINSTOCK C.,
 RA WILKINSON-SPOAT J., WOHLDMAN P.,
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans."
 RL NATURE 368:32-38(1994).
 DR EMBL: 258214: E1321758;
 DR EMBL: 259062: E1321758; JOINED.
 DR EMBL: 259442: E1322835;
 DR EMBL: 258214: E1322835; JOINED.
 SC SEQUENCE 1763 AA: 201072 MW: FEDA34C5 CPC32;

Query Match 87.18; Score 27; DB 3; Length 1763;
 Best Local Similarity 83.38; Fred. No. 4.1e-02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NDOVLF 6
 11111
 Db 183 NDRYLF 188

Search completed: June 22, 1999, 11:01:19
 Job time: 165 sec



GenGene version 4.1
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OM protein - protein search, using SW model

Run on: June 22, 1999, 10:58:34 : Search time 45.16 seconds
(without alignments)
3.566 Million cell updates/sec

Title: US-09-030-061-1
Period: 1999-01-01
Sequence: 1 NCVLF 6
Scoring table: EIGENM2
Search: 1400 seqs, 2680235 residues
Database: 3.566M cell updates/sec

File: The number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No	Score	Query Match	Length	DB ID	Description
1	100	100	1	1118_HUMAN	G14116 homo sapien
2	100	100	1	1118_MOUSE	P70940 mus musculu
3	100	100	1	1118_PRT	P70940 sus domest
4	100	100	1	1118_PRT	P70940 sus domest
5	100	100	1	1118_PRT	P70940 sus domest
6	100	100	1	1118_PRT	P70940 sus domest
7	100	100	1	1118_PRT	P70940 sus domest
8	100	100	1	1118_PRT	P70940 sus domest
9	100	100	1	1118_PRT	P70940 sus domest
10	100	100	1	1118_PRT	P70940 sus domest
11	100	100	1	1118_PRT	P70940 sus domest
12	100	100	1	1118_PRT	P70940 sus domest
13	100	100	1	1118_PRT	P70940 sus domest
14	100	100	1	1118_PRT	P70940 sus domest
15	100	100	1	1118_PRT	P70940 sus domest
16	100	100	1	1118_PRT	P70940 sus domest
17	100	100	1	1118_PRT	P70940 sus domest
18	100	100	1	1118_PRT	P70940 sus domest
19	100	100	1	1118_PRT	P70940 sus domest
20	100	100	1	1118_PRT	P70940 sus domest
21	100	100	1	1118_PRT	P70940 sus domest
22	100	100	1	1118_PRT	P70940 sus domest
23	100	100	1	1118_PRT	P70940 sus domest
24	100	100	1	1118_PRT	P70940 sus domest
25	100	100	1	1118_PRT	P70940 sus domest
26	100	100	1	1118_PRT	P70940 sus domest
27	100	100	1	1118_PRT	P70940 sus domest
28	100	100	1	1118_PRT	P70940 sus domest
29	100	100	1	1118_PRT	P70940 sus domest
30	100	100	1	1118_PRT	P70940 sus domest
31	100	100	1	1118_PRT	P70940 sus domest
32	100	100	1	1118_PRT	P70940 sus domest
33	100	100	1	1118_PRT	P70940 sus domest
34	100	100	1	1118_PRT	P70940 sus domest
35	100	100	1	1118_PRT	P70940 sus domest
36	100	100	1	1118_PRT	P70940 sus domest
37	100	100	1	1118_PRT	P70940 sus domest
38	100	100	1	1118_PRT	P70940 sus domest
39	100	100	1	1118_PRT	P70940 sus domest
40	100	100	1	1118_PRT	P70940 sus domest
41	100	100	1	1118_PRT	P70940 sus domest
42	100	100	1	1118_PRT	P70940 sus domest
43	100	100	1	1118_PRT	P70940 sus domest

ALIGNMENTS

Result ID	Query Match	Length	DB ID	Description
1	100	100	1118_HUMAN	G14116 homo sapien
2	100	100	1118_MOUSE	P70940 mus musculu
3	100	100	1118_PRT	P70940 sus domest
4	100	100	1118_PRT	P70940 sus domest
5	100	100	1118_PRT	P70940 sus domest
6	100	100	1118_PRT	P70940 sus domest
7	100	100	1118_PRT	P70940 sus domest
8	100	100	1118_PRT	P70940 sus domest
9	100	100	1118_PRT	P70940 sus domest
10	100	100	1118_PRT	P70940 sus domest
11	100	100	1118_PRT	P70940 sus domest
12	100	100	1118_PRT	P70940 sus domest
13	100	100	1118_PRT	P70940 sus domest
14	100	100	1118_PRT	P70940 sus domest
15	100	100	1118_PRT	P70940 sus domest
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18	100	100	1118_PRT	P70940 sus domest
19	100	100	1118_PRT	P70940 sus domest
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33	100	100	1118_PRT	P70940 sus domest
34	100	100	1118_PRT	P70940 sus domest
35	100	100	1118_PRT	P70940 sus domest
36	100	100	1118_PRT	P70940 sus domest
37	100	100	1118_PRT	P70940 sus domest
38	100	100	1118_PRT	P70940 sus domest
39	100	100	1118_PRT	P70940 sus domest
40	100	100	1118_PRT	P70940 sus domest
41	100	100	1118_PRT	P70940 sus domest
42	100	100	1118_PRT	P70940 sus domest
43	100	100	1118_PRT	P70940 sus domest

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01 15-JUL-1994 (REL. 36, LAST SEQUENCE CREATED)
02 15-JUL-1994 (REL. 36, LAST ANNOTATION UPDATE)
03 INTERLEUKIN-18 PROCURSOR (IL-18) (INTERFERON-GAMMA INDUCING FACTOR)
04 DE (VIR-GAMMA-INDUCING FACTOR) (INTERLEUKIN 1 GENE) (VIR-GAMMA)
05 IL18 OR IGIF.
06 RATIUS NOREVICIUS (RAT)
07 ERYTHROCYTE, METAZOON, CHELATA, VERTEBRATA, MAMMALIA
08 EUTHERIA, RODENTIA.
09
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12 SEQUENCE FROM N.A.
13 STRAIN=SPRAGUE-DAWLEY; TISSUE=ADRENAL GLAND;
14 MEDLINE: 97152963.
15
16 CONTI B., SAHNG J.W., TINI C., SON J.H., JOH L.H.
17 R. J. BIOL. CHEM. 272:2025-2037(1997)
18
19 -1- FUNCTION: ADRENAL NADPHAL KILLER CELL ACTIVITY IN SPLEN CELLS
20 AND STIMULATES INTERFERON GAMMA PRODUCTION IN 1 HELPER TYPE 1
21 CELLS
22
23 EMBL: 077776; G1809129;
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25 EMBL: 077777; G1809131;
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27 CYTOKINE; ALTERNATIVE SPLICING.
28
29 PROPEP 1 36 BY SIMILARITY.
30
31 CHAIN 37 193 INTERLEUKIN-18.
32
33 VARSPLIC 121 139 MISSING (IN ISOFORM ALPHA).
34
35 SEQUENCE 194 AA; 22983 WS; 9497.21 *9022.
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FT	SIGNAL	1	42	POTENTIAL.
FT	CHAIN	43	769	INTERIN BETA-8.
FT	CHAIN	42	694	EXTRACELLULAR (POTENTIAL).
FT	CHAIN	42	704	POTENTIAL.
FT	TRANSMEM	685	759	POTENTIAL.
FT	CHAIN	705	759	CHOLASMIC (POTENTIAL).
FT	CHAIN	471	629	CHOLASMIC (POTENTIAL).
FT	REPEAT	471	510	CHOLASMIC (POTENTIAL).
FT	REPEAT	511	552	CHOLASMIC (POTENTIAL).
FT	REPEAT	552	592	CHOLASMIC (POTENTIAL).
FT	REPEAT	592	632	CHOLASMIC (POTENTIAL).
FT	REPEAT	632	672	CHOLASMIC (POTENTIAL).
FT	REPEAT	672	712	CHOLASMIC (POTENTIAL).
FT	REPEAT	712	752	CHOLASMIC (POTENTIAL).
FT	REPEAT	752	792	CHOLASMIC (POTENTIAL).
FT	REPEAT	792	832	CHOLASMIC (POTENTIAL).
FT	REPEAT	832	872	CHOLASMIC (POTENTIAL).
FT	REPEAT	872	912	CHOLASMIC (POTENTIAL).
FT	REPEAT	912	952	CHOLASMIC (POTENTIAL).
FT	REPEAT	952	992	CHOLASMIC (POTENTIAL).
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FT	REPEAT	1032	1072	CHOLASMIC (POTENTIAL).
FT	REPEAT	1072	1112	CHOLASMIC (POTENTIAL).
FT	REPEAT	1112	1152	CHOLASMIC (POTENTIAL).
FT	REPEAT	1152	1192	CHOLASMIC (POTENTIAL).
FT	REPEAT	1192	1232	CHOLASMIC (POTENTIAL).
FT	REPEAT	1232	1272	CHOLASMIC (POTENTIAL).
FT	REPEAT	1272	1312	CHOLASMIC (POTENTIAL).
FT	REPEAT	1312	1352	CHOLASMIC (POTENTIAL).
FT	REPEAT	1352	1392	CHOLASMIC (POTENTIAL).
FT	REPEAT	1392	1432	CHOLASMIC (POTENTIAL).
FT	REPEAT	1432	1472	CHOLASMIC (POTENTIAL).
FT	REPEAT	1472	1512	CHOLASMIC (POTENTIAL).
FT	REPEAT	1512	1552	CHOLASMIC (POTENTIAL).
FT	REPEAT	1552	1592	CHOLASMIC (POTENTIAL).
FT	REPEAT	1592	1632	CHOLASMIC (POTENTIAL).
FT	REPEAT	1632	1672	CHOLASMIC (POTENTIAL).
FT	REPEAT	1672	1712	CHOLASMIC (POTENTIAL).
FT	REPEAT	1712	1752	CHOLASMIC (POTENTIAL).
FT	REPEAT	1752	1792	CHOLASMIC (POTENTIAL).
FT	REPEAT	1792	1832	CHOLASMIC (POTENTIAL).
FT	REPEAT	1832	1872	CHOLASMIC (POTENTIAL).
FT	REPEAT	1872	1912	CHOLASMIC (POTENTIAL).
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FT	REPEAT	1952	1992	CHOLASMIC (POTENTIAL).
FT	REPEAT	1992	2032	CHOLASMIC (POTENTIAL).
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FT	REPEAT	2112	2152	CHOLASMIC (POTENTIAL).
FT	REPEAT	2152	2192	CHOLASMIC (POTENTIAL).
FT	REPEAT	2192	2232	CHOLASMIC (POTENTIAL).
FT	REPEAT	2232	2272	CHOLASMIC (POTENTIAL).
FT	REPEAT	2272	2312	CHOLASMIC (POTENTIAL).
FT	REPEAT	2312	2352	CHOLASMIC (POTENTIAL).
FT	REPEAT	2352	2392	CHOLASMIC (POTENTIAL).
FT	REPEAT	2392	2432	CHOLASMIC (POTENTIAL).
FT	REPEAT	2432	2472	CHOLASMIC (POTENTIAL).
FT	REPEAT	2472	2512	CHOLASMIC (POTENTIAL).
FT	REPEAT	2512	2552	CHOLASMIC (POTENTIAL).
FT	REPEAT	2552	2592	CHOLASMIC (POTENTIAL).
FT	REPEAT	2592	2632	CHOLASMIC (POTENTIAL).
FT	REPEAT	2632	2672	CHOLASMIC (POTENTIAL).
FT	REPEAT	2672	2712	CHOLASMIC (POTENTIAL).
FT	REPEAT	2712	2752	CHOLASMIC (POTENTIAL).
FT	REPEAT	2752	2792	CHOLASMIC (POTENTIAL).
FT	REPEAT	2792	2832	CHOLASMIC (POTENTIAL).
FT	REPEAT	2832	2872	CHOLASMIC (POTENTIAL).
FT	REPEAT	2872	2912	CHOLASMIC (POTENTIAL).
FT	REPEAT	2912	2952	CHOLASMIC (POTENTIAL).
FT	REPEAT	2952	2992	CHOLASMIC (POTENTIAL).
FT	REPEAT	2992	3032	CHOLASMIC (POTENTIAL).
FT	REPEAT	3032	3072	CHOLASMIC (POTENTIAL).
FT	REPEAT	3072	3112	CHOLASMIC (POTENTIAL).
FT	REPEAT	3112	3152	CHOLASMIC (POTENTIAL).
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RESULT 8
MPOC.MVGC ID MPOC.MVGC STANDARD: pnt: 1052 AA
A: 72737 267491 267498 247254 247395 249257:
GT 01-AUG-1991 (PEL: 19) CREATED)
GT 01-AUG-1991 (PEL: 19) LAST SEQUENCE UPDATE)
GT 01-NOV-1997 (PEL: 35) LAST ANNOTATION UPDATE)
DE MPOC PROTEIN PRECURSOR.
MPOC OR MG192.
OS MYOPLASMA GENITALIUM.
OS PRAKARYOTA, TEMPFIDELIS, MLLIDIES: MYOPLASMA MPOC(MYMALES)
OC MYOPLASMAICAEAE.
RN RN
RP SEQUENCE FROM N.A.
R1 STRAIN:ALC 33510 / G-37:
R2 MEDLINE: 900609815.
RA INAMINE J.M., LOECHEL S., COLLIER A.M., BARILE M.F., HU P.-C.:
GENE 92-260-267(1989).
R1 PI 12
R2 SEQUENCE FROM N.A.
R1 STRAIN:ALC 33510 / G-37:
R2 MEDLINE: 900609815.
RA INAMINE J.M., LOECHEL S., COLLIER A.M., BARILE M.F., HU P.-C.:
GENE 92-260-267(1989).
RN RN
RP SEQUENCE FROM N.A.
R1 STRAIN:ALC 33510 / G-37:
R2 MEDLINE: 900609815.
RA FRAGER G.M., BOGAVANT D., WHITE G., ADAMS M.D., CLAYTON R.A.,
FELTSCHMANN F.D., HOLT J.T., PERLWADZ A., FOLSTEN G., KELLY C.M.,
FELTSCHMANN F.D., WEIDMAN J.L., SMALL R.V., SANDERS M., FORHRANN J.L.,
NAYEN T.F., OFFERVAULT P., SAGERT E.M., PHILLIPS C.A., MEDERICK L.M.,
TOWSE J.F., TROTSKY P.A., BOTT F.F., HU P.-C.: JOURNAL OF
PETERSON S.N., SMITH H.B., HEDRICHSON C.A. III, VENTER J.C.:
SCIENT 200337-40(1993).
RN RN
RP SEQUENCE OF 50-1571 200337-44(1993) AND 364-1052.
R1 STRAIN:ALC 33510 / G-37:
R2 MEDLINE: 91075930.
RA PETERSON S.N., HU P.-C., BOTT F.F., HUTCHISON C.A. III:
J. BACTERIOL. 175(1918-7930(1993)).
RN RN
RP SEQUENCE OF 759-954 FROM N.A.
R1 STRAIN:ALC 33510 / G-37:
R2 MEDLINE: 92051936.
RA PETERSON S.N., SCHWAB M., HU P.-C., BOTT F.F., HUTCHISON C.A. III:
NUCLEIC ACIDS RES. 19-5037-5031(1991).
DE EMBL: M14311 G1501660-
EMBL: 014936 1147377-
EMBL: 202124 G409890-

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Genstat version 4.5
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OM protein - protein search, using sw model

Run on: Time 22. 1999. 10:56:38. Search time 61.72 seconds

(without alignments)
1.966 Million cell updates/sec

Title: US-09-030-061-2

Perfect score: 33

Sequence: 1 PEDMTD 6

Scoring table: BLOSUM62

Sw-Model: 1999-03-18. 1999-03-18. 1999-03-18

Database: A_Genoseq_34:*

Prod No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	33	100.0	18	P92505	Interferon gamma F
2	32	100.0	157	P92506	Interferon gamma F
3	32	100.0	157	P92564	Human interferon-gamma
4	32	100.0	157	P92558	Human mature inter
5	32	100.0	157	P92558	Human mature inter
6	32	100.0	157	P92560	Human mature inter
7	32	100.0	157	P92562	Human mature inter
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16	32	100.0	157	P92562	Human mature inter
17	32	100.0	157	P92562	Human mature inter
18	32	100.0	157	P92562	Human mature inter
19	32	100.0	157	P92562	Human mature inter
20	32	100.0	157	P92562	Human mature inter
21	32	100.0	157	P92562	Human mature inter
22	32	100.0	157	P92562	Human mature inter
23	32	100.0	157	P92562	Human mature inter
24	32	100.0	157	P92562	Human mature inter
25	32	100.0	157	P92562	Human mature inter
26	32	100.0	157	P92562	Human mature inter
27	32	100.0	157	P92562	Human mature inter
28	32	100.0	157	P92562	Human mature inter
29	32	100.0	157	P92562	Human mature inter
30	32	100.0	157	P92562	Human mature inter
31	32	100.0	157	P92562	Human mature inter
32	32	100.0	157	P92562	Human mature inter
33	32	100.0	157	P92562	Human mature inter
34	32	100.0	157	P92562	Human mature inter
35	32	100.0	157	P92562	Human mature inter
36	32	100.0	157	P92562	Human mature inter
37	32	100.0	157	P92562	Human mature inter
38	32	100.0	157	P92562	Human mature inter
39	32	100.0	157	P92562	Human mature inter
40	32	100.0	157	P92562	Human mature inter
41	32	100.0	157	P92562	Human mature inter
42	32	100.0	157	P92562	Human mature inter
43	32	100.0	157	P92562	Human mature inter
44	32	100.0	157	P92562	Human mature inter
45	32	100.0	157	P92562	Human mature inter

ALIGNMENTS

RESULT 1

ID P92505 standard: Peptide: 18 AA.

DE Interferon gamma production induced peptide #2.

KW Interferon gamma inducer IFN-gamma, immunocompetent cell: antiviral;

KW antitumor; antileptotic; immunoregulatory; platelet-increasing agent;

KW therapy; prevention; solid tumor accumulation; renal cancer; brain cancer;

KW granuloma; mycosis; (antibiotic) rheumatism; allergy; cytotoxicity; AIDS;

KW killer T-cell; interleukin-2; IL-2; tumor necrosis factor; TNF;

KW adoptive immunotherapy; monoclonal antibody.

OS Synthetic.

PI Kohn K, Kunkata T, Kurimoto M, Okamura H, Taniguchi M.

PI Yamamoto T, Toriige K.

PI WPI: 96-070177/08.

PI Protein that induces gamma interferon production in immunocompetent

PI cells, used e.g. as activator of antitumor agent, also induces

PI cytotoxicity of killer cells.

PI Chain: 1-18, 33pp, English.

PI P92504 and P92505 represent fragments of the protein of the invention

PI (see P92506), which induces interferon gamma (IFN-gamma) production in

PI immunocompetent cells. The protein is useful as an antiviral.

PI antitumor, antileptotic, immunoregulatory and platelet-increasing agent.

PI It can be used for treating: rheumatism; arthritis; rheumatoid arthritis;

PI renal or brain cancer; granuloma; mycosis; leukemia; hemophilia and

PI allergy. The protein can also be used to induce IFN-gamma production in

PI cultured cells. The IFN-gamma inducer strongly induces cytotoxicity of

PI killer T-cells and when used with interleukin-2 (IL-2) and tumour

PI necrosis factor (TNF) may improve the effect (or reduce side effects) of

PI adoptive immunotherapy in tumours. The RNA encoding this protein (see

PI P92504) can be used to produce the protein, which can then be purified

PI (or assayed) using monoclonal antibodies.

PI Sequence: 18 AA.

PI Query Match: 100.0%, Score 33, DB: Length 18;

PI Best local similarity: 100.0%; Prod No. 92505;

PI Multiple K: 1; Misassembly: 0; Mismatches: 0; Gaps: 0.

PI Query: 1 PEDMTD 6

PI DB: 4 PEDMTD 9

PI RESULT 2

PI ID P92506 standard: Protein: 157 AA.

AC P92506;

DE 02-SEP-1996 (first entry)

DE Interferon gamma production induced protein.

KW Interferon gamma inducer IFN-gamma, immunocompetent cell: antiviral;

KW antitumor; antileptotic; immunoregulatory; platelet-increasing agent;

KW therapy; prevention; solid tumor accumulation; renal cancer; brain cancer;

KW granuloma; mycosis; (antibiotic) rheumatism; allergy; cytotoxicity; AIDS;

KW killer T-cell; interleukin-2; IL-2; tumour necrosis factor; TNF;

KW adoptive immunotherapy; monoclonal antibody.

OS Mus musculus.

PI Key: Location: Qualifiers

PI Misc_difference: 70

ID R99550 standard; Protein: 157 AA.
 AC R99550;
 DT 29-SEP-1996 (first entry)
 DE Mouse gamma interferon protein inducer protein.
 KM Interferon gamma inducer protein; IFN-gamma, antiviral, virocidic,
 KM anti-tumor, antitubercular, immunoregulatory, adoptive immunotherapy;
 KM thymic cancer.
 OS Mus sp.
 PE 10-NOV-1995: 308055.
 PR 15-NOV-1994: JP-304203.
 PR 22-SEP-1995: JP-262062.
 PR 10-MAR-1995: JP-078357.
 PR 18-SEP-1995: JP-262062.
 PR 23-SEP-1995: JP-274988.
 PA (HAYAB) HAYASHIBARA SEIBUTSU KAGAKU.
 PI Furuda S, Kohno K, Kunitada T, Kurimoto M, Okamura H,
 PI Taniguchi M, Taniguchi T, Torigoe K, Ushio S,
 DR N-PSDB: 132403.
 DR N-PSDB: 132403.
 PT DNA encoding interferon gamma protein-inducing polypeptide: useful
 PI to treat and prevent, e.g. viral disease, malignancies and immune
 PI disorders.
 PS Example A-3-2: Page 36-37, 18pp. English.
 CC A novel mouse protein (R99550) induces interferon-gamma (IFN-gamma)
 CC protein by immunocompetent cells. Its sequence was deduced from
 CC that of a cDNA clone (132403) isolated from a mouse liver library.
 CC Protein-induced interferon protein can be produced in high yields
 CC using host cells, esp. Escherichia coli, transformed with a vector
 CC carrying the cDNA.
 CC Sequence: 157 AA.
 SQ Sequence: 157 AA.
 Query Match: 100.0%; Score: 33; DB: 1; Length: 157;
 Best local similarity: 100.0%; Prod. No. 2.7;
 Matches: 6; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;
 OY 1 FEDMTD 6
 DB 29 FEDMTD 14
 RESULT 6
 R99560
 ID R99560 standard; Protein: 193 AA.
 AC R99560;
 DT 29-SEP-1996 (first entry)
 DE Human interferon gamma inducer protein.
 KM Interferon gamma inducer protein; IFN-gamma, antiviral, virocidic,
 KM antitumor, antitubercular, immunoregulatory, adoptive immunotherapy;
 KM thymic cancer.
 OS Homo sapiens.
 PE 10-NOV-1995: 308055.
 PR 15-NOV-1994: JP-304203.
 PR 22-SEP-1995: JP-262062.
 PR 10-MAR-1995: JP-078357.
 PR 18-SEP-1995: JP-262062.
 PR 23-SEP-1995: JP-274988.
 PA (HAYAB) HAYASHIBARA SEIBUTSU KAGAKU.
 PI Furuda S, Kohno K, Kunitada T, Kurimoto M, Okamura H,
 PI Taniguchi M, Taniguchi T, Torigoe K, Ushio S,
 DR N-PSDB: 132403.
 DR N-PSDB: 132403.
 PT DNA encoding interferon gamma protein-inducing polypeptide: useful
 PI to treat and prevent, e.g. viral disease, malignancies and immune
 PI disorders.
 PS Example A-3-2: Page 36-37, 18pp. English.
 CC A novel mouse protein (R99560) induces interferon-gamma (IFN-gamma)
 CC protein by immunocompetent cells. Its sequence was deduced from
 CC that of a cDNA clone (132403) isolated from a mouse liver library.
 CC Protein-induced interferon protein can be produced in high yields
 CC using host cells, esp. Escherichia coli, transformed with a vector
 CC carrying the cDNA.
 CC Sequence: 193 AA.
 SQ Sequence: 193 AA.
 Query Match: 100.0%; Score: 33; DB: 1; Length: 157;
 Best local similarity: 100.0%; Prod. No. 2.7;
 Matches: 6; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;
 OY 1 FEDMTD 6
 DB 29 FEDMTD 14

PI Taniguchi M, Taniguchi T, Torigoe K, Ushio S,
 DR N-PSDB: 132404.
 DE DNA encoding interferon gamma protein-inducing polypeptide: useful
 PI to treat and prevent, e.g. viral disease, malignancies and immune
 PI disorders.
 PS Claim 6, Page 41-42, 48pp. English.
 CC The major portion of a novel human protein (R99560) induces
 CC interferon gamma (IFN-gamma) protein by immunocompetent cells. It
 CC is the product of a cDNA clone (132404) obtained from a human liver
 CC library. The protein induces the cytotoxicity of killer cells
 CC and/or induces the formation of killer cells (e.g. NK cells,
 CC lymphokine-activated killer (LAK) cells, and cytotoxic T-cells).
 CC The mouse protein (see also R99550) is useful as an antiviral,
 CC antitumor, antitubercular, immunoregulatory and blood protein.
 CC The protein can be used to produce immunoregulatory. It is
 CC also used to raise monoclonal antibodies.
 CC Sequence: 193 AA.
 SQ Sequence: 193 AA.

Query Match: 100.0%; Score: 33; DB: 1; Length: 18;
 Best local similarity: 100.0%; Prod. No. 3.4;
 Matches: 6; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;
 OY 1 FEDMTD 6
 DB 66 FEDMTD 71
 RESULT 7
 R99562
 ID R99562 standard; Protein: 18 AA.
 AC R99562;
 DT 29-SEP-1996 (first entry)
 DE Human interferon gamma inducer protein (IFN-gamma, antiviral, virocidic,
 KM antitumor, antitubercular, immunoregulatory, adoptive immunotherapy;
 KM thymic cancer).
 OS Mus sp.
 PE 10-NOV-1995: 308055.
 PR 15-NOV-1994: JP-304203.
 PR 23-FEB-1995: JP-058240.
 PR 10-MAR-1995: JP-078357.
 PR 18-SEP-1995: JP-262062.
 PR 23-SEP-1995: JP-274988.
 PA (HAYAB) HAYASHIBARA SEIBUTSU KAGAKU.
 PI Furuda S, Kohno K, Kunitada T, Kurimoto M, Okamura H,
 PI Taniguchi M, Taniguchi T, Torigoe K, Ushio S,
 DR N-PSDB: 132403.
 DR N-PSDB: 132403.
 PT DNA encoding interferon gamma protein-inducing polypeptide: useful
 PI to treat and prevent, e.g. viral disease, malignancies and immune
 PI disorders.
 PS Example A-3-6: Page 17, 48pp. English.
 CC Hypuric peptides (R99561 and R99562) correspond to amino acids
 CC 39-110 and 10-43, respectively, of a novel interferon-gamma
 CC (IFN-gamma) inducer protein identified in mouse liver. The
 CC peptide's amino acid sequence, PFF PFF PFF PFF PFF PFF PFF PFF PFF
 CC (111) is in the amino acid sequence of mouse liver cDNA. Leading to
 CC the isolation of a cDNA (132403) coding for mouse IFN-gamma
 CC inducer protein (R99559).
 CC Sequence: 18 AA.
 SQ Sequence: 18 AA.

Query Match: 100.0%; Score: 33; DB: 1; Length: 18;
 Best local similarity: 100.0%; Prod. No. 3.4;
 Matches: 6; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;
 OY 1 FEDMTD 6
 DB 4 FEDMTD 9

RESULT 11
 W24258
 AC W24258 standard; Protein; 157 AA.
 DT 15-OCT-1997 (first entry)
 DE Interferon gamma inducing factor-2 (IGIF-2) R1401 variant.
 KW Interferon gamma inducing factor-2 (IGIF-2) variant; lymphocyte human; bacterial infection; malignant tumour; viral diseases; bacterial infection; immune disease.
 OS Homo sapiens.
 FH Key.
 FT misc_difference 73
 /note= "Encoded by AY1"
 FT 1
 FN J09157180-A.
 PD 17-JUN-1997.
 PF 24-JAN-1995; 028722.
 PR 04-OCT-1995; JP-279906.
 PR 10-MAR-1995; JP-078357.
 PR 29-SEP-1995; JP-274988.
 PA (HAYB.) HAYASHIHARA SEIBUTSU KAGAKU.
 DP WPI: 97-369391/34.
 DK N-PSDB: 180209.
 FT A drug containing a polypeptide which induces interferon-gamma
 PT useful for treating e.g. malignant tumours, viral, bacterial or
 immune diseases.
 PS Claim 1: Page 9; 12pp; Japanese.
 CC This sequence represents a protein which induces interferon-gamma
 CC production in immunocompetent cells. This protein may be used as
 CC the major component in a drug for the prevention and treatment of
 CC e.g. malignant tumours, viral diseases, bacterial infections and
 CC immune diseases.
 SC Sequence 157 AA.
 CY 1 FEDMTD 6
 ID 30 FEDMTD 35
 DB 30 FEDMTD 35
 RESULT 11
 W31757
 AC W31757 standard; Protein; 193 AA.
 DT 15-JAN-1998 (first entry)
 DE Interferon gamma inducing factor-2 (IGIF-2) R1401 variant.
 KW Interferon gamma inducing factor-2 (IGIF-2) variant; lymphocyte human; bacterial infection; malignant tumour; viral diseases; bacterial infection; immune disease.
 OS Homo sapiens.
 FH Key.
 FT misc_difference 140
 /label= R1401
 /note= "Wild type Arg 15 is replaced by Ile"
 FT 1
 FN W0974441-A1.
 PD 10-JUL-1997.
 PF 29-DEC-1995; 020432.
 PR 29-DEC-1995; US-580667.
 PA (TNEY-) INCYTE PHARM INC.
 PI Corcks RG; Coleman R; Hawkins PR.
 DR N-PSDB: T74988.
 PT Novel interferon gamma inducing factor-2 - used to screen for compounds to diagnose, treat or prevent tissue damage associated

Best Local Similarity 100.0%; Pred. No. 0.26;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0
 CY 1 FEDMTD 6
 ID 30 FEDMTD 9
 DB 4 FEDMTD 9
 RESULT 10
 W24258
 AC W24258 standard; Protein; 157 AA.
 DT 15-OCT-1997 (first entry)
 DE Human protein for induction of interferon-gamma.
 KW Interferon-gamma; immunocompetent cell; malignant tumour;
 KW viral diseases; bacterial infection; immune disease.
 OS Homo sapiens.
 FH Key.
 FT misc_difference 73
 /note= "Encoded by AY1"
 FT 1
 FN J09157180-A.
 PD 17-JUN-1997.
 PF 24-JAN-1995; 028722.
 PR 04-OCT-1995; JP-279906.
 PR 10-MAR-1995; JP-078357.
 PR 29-SEP-1995; JP-274988.
 PA (HAYB.) HAYASHIHARA SEIBUTSU KAGAKU.
 DP WPI: 97-369391/34.
 DK N-PSDB: 180209.
 FT A drug containing a polypeptide which induces interferon-gamma
 PT useful for treating e.g. malignant tumours, viral, bacterial or
 immune diseases.
 PS Claim 1: Page 9; 12pp; Japanese.
 CC This sequence represents a protein which induces interferon-gamma
 CC production in immunocompetent cells. This protein may be used as
 CC the major component in a drug for the prevention and treatment of
 CC e.g. malignant tumours, viral diseases, bacterial infections and
 CC immune diseases.
 SC Sequence 157 AA.
 CY 1 FEDMTD 6
 ID 30 FEDMTD 35
 DB 30 FEDMTD 35
 RESULT 11
 W31757
 AC W31757 standard; Protein; 193 AA.
 DT 15-JAN-1998 (first entry)
 DE Interferon gamma inducing factor-2 (IGIF-2) R1401 variant.
 KW Interferon gamma inducing factor-2 (IGIF-2) variant; lymphocyte human; bacterial infection; malignant tumour; viral diseases; bacterial infection; immune disease.
 OS Homo sapiens.
 FH Key.
 FT misc_difference 140
 /label= R1401
 /note= "Wild type Arg 15 is replaced by Ile"
 FT 1
 FN W0974441-A1.
 PD 10-JUL-1997.
 PF 29-DEC-1995; 020432.
 PR 29-DEC-1995; US-580667.
 PA (TNEY-) INCYTE PHARM INC.
 PI Corcks RG; Coleman R; Hawkins PR.
 DR N-PSDB: T74988.
 PT Novel interferon gamma inducing factor-2 - used to screen for compounds to diagnose, treat or prevent tissue damage associated

PT With inflammation
PS Claim 3: Page 1: 50pp; English.
CC This protein sequence represents an interferon gamma inducing factor-2 (IGIF-2) variant, identified from a liver cDNA library. This sequence differs from IGIF-2 identified from a T-lymphocyte cDNA library (W22047), in that amino acid 140 is found to be changed from Arg to Ile. A second variant, W22049, also exists. Probes derived from the nucleic acid sequences can be used to quantify the expression of IGIF-2 in conditions that are associated with inflammation or aberrant expression of IGIF-2.
CC The protein can be used to screen for compounds that interact with IGIF-2, such as inhibitors of other cell lines (especially fibrocytes or antileukemic sequences) of IGIF-2 expression or activity. The protein can also be used to diagnose, prevent or treat IGIF-2 induction of proliferation, differentiation or maturation of leukocytes or lymphocytes, especially in relation to tissue damage associated with inflammation.
CC These amino acid sequences have not appear in the specification. It has been established that the IGIF-2 sequence presented in W22047 is Sequence 133 AA.

Query Match 100.0% Score 33 DB 1 Length 193
Best Local Similarity 100.0% Prod. No. 3.4
Matches 6: Conservative 0: Mismatches 0: Indels 0 Gaps 0

QY 1 FEDMD 6
DB 56 FEDMD 71

RESULT 12
ID W22047
AC W22047
DE 14-JAN-1998 (first entry)
DE Interferon gamma inducing factor-2 (IGIF-2) protein.
KW Interferon gamma inducing factor-2, IGIF-2, leukocyte, lymphocyte, inflammation, proliferation, differentiation, maturation, tissue damage, human.
OS Homo sapiens.
PN W0972441-A1
PD 10-SEP-1997
PR 20-SEP-1996 JP-269105
PA (NCRV) INOYE PHARM. INC.
PI Cocke R, Coleman P, Hawkins P;
DR WPI: 97-363677/33.
DR N-PSDB: T74987.
PT Novel interferon gamma inducing factor-2 - used to screen for compounds to diagnose, treat or prevent tissue damage associated with inflammation
PS Claim 1: Page 43: 50pp; English.
CC This is the protein sequence of interferon gamma inducing factor-2 (IGIF-2). An IGIF-2 variant (W22049) and an IGIF variant (W22049), which may be an alternative transcript, also exist. Probes derived from the nucleic acid sequences can be used to quantify the expression of IGIF-2 in conditions that are associated with inflammation or aberrant expression of IGIF-2. The protein can be used to screen for compounds that interact with IGIF-2, such as antibodies, antagonists or other inhibitors (especially antibodies or antileukemic sequences) of IGIF-2 expression. Similarly, the protein can also be used to diagnose, prevent or treat IGIF-2 induction of proliferation, differentiation or maturation of leukocytes or lymphocytes, especially in relation to tissue damage associated with inflammation.
CC Sequence 193 AA.

Query Match 100.0% Score 33 DB 1 Length 193
Best Local Similarity 100.0% Prod. No. 3.4
Matches 6: Conservative 0: Mismatches 0: Indels 0 Gaps 0

QY 1 FEDMD 6
DB 56 FEDMD 71

DB 56 FEDMD 71

RESULT 13
ID W15704
AC W15704
DE 26-JAN-1999 (first entry)
DE Mouse interferon-gamma inducer protein.
KW Interferon-gamma, IFN-gamma, antiviral, antineoplastic, radiotherapy, immunomodulatory, cell growth agent, chemokine, leukopenia, thrombocytopenia, immunocompetent cells, asthma, hayfever, rheumatism, interleukin, Miller cell.
OS Mus musculus.
PT Key Location/Qualifiers
FT Misc-difference 70
FT /label Mot, Thr
FN EF-76778-A1
PD 09-APR-1997
PR 26-SEP-1996 JP-269105
PR 26-SEP-1996 JP-270725
PR 29-FEB-1998 JP-067434.
PA (HAYS) HAYASHI/DAVA SEIBUTSU KAKAYU.
PI Akita K, Fujii M, Kurimoto M, Nakada Y, Tanimoto T;
DR WPI: 97-205381/15.
DR N-PSDB: T60536.
PT Human protein that induces interferon-gamma prodn. in immunocompetent cells - useful for adoptive immunotherapy of tumors and as antimicrobial agent etc.
PS Disclosure, page 22, 25pp, English.
CC The present sequence represents a novel protein from mouse liver cells, which induces interferon-gamma (IFN-gamma) production in immunocompetent cells. This protein enhances cytotoxicity of killer cells and induces their formation. It is used as an antileukemic agent for anti-tumor immunotherapy, an antiviral (including anti-AIDS) or antibacterial agent, and in the treatment of allergic immune system disorders, e.g. asthma, hayfever or rheumatism. When formulated with interleukin-3, it is also used to treat leukopenia and thrombocytopenia associated with radiotherapy or chemotherapy of leukemia and other cancers. When used in autotumor immunotherapy, this novel protein significantly improves the therapeutic effect of interferon-gamma. This protein is used for the treatment of cancer when administered to the patient (before administration of IFN-3) or by addition to the medium in which cells (intended for return to the patient) are being grown.
CC Sequence 197 AA.

Query Match 100.0% Score 33 DB 1 Length 193
Best Local Similarity 100.0% Prod. No. 2.7
Matches 6: Conservative 0: Mismatches 0: Indels 0 Gaps 0

QY 1 FEDMD 6
DB 29 FEDMD 34

RESULT 14
ID W15697
AC W15697
DE 26-JAN-1999 (first entry)
DE N-terminal fragment of interferon gamma inducer protein.
KW Interferon-gamma, IFN-gamma, antiviral, antineoplastic, radiotherapy, immunomodulatory, cell growth agent, chemokine, leukopenia, thrombocytopenia, immunocompetent cells, asthma, hayfever, rheumatism, interleukin, Miller cell.
OS Homo sapiens.
PN EF-76778-A1
PD 09-APR-1997
PR 26-SEP-1996 JP-269105
PR 20-SEP-1996 JP-270725.
PR 26-SEP-1996 JP-270725.

1	170	0	192	2	cytokine IGIF -
2	30	80.9	348	2	sensory transduct
3	30	80.9	59036	2	hypothetical prot
4	30	80.9	59087	2	HXA12 protein - h
5	30	80.9	338	2	excision repair p
6	29	87.9	754	1	ATP-binding prote
7	29	87.9	1071	2	hypothetical prot
8	29	87.9	34378	2	fibronectin bindi
9	29	87.9	910	2	RNA-binding PNA1
10	29	87.9	1357	2	transcription inh
11	29	87.9	482	2	phosphoprotein
12	29	87.9	446	2	phosphoprotein
13	29	87.9	446	2	conserved hypot
14	29	87.9	363	2	conserved hypot
15	29	87.9	363	2	conserved hypot
16	29	87.9	363	2	conserved hypot
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22	29	87.9	363	2	conserved hypot
23	29	87.9	363	2	conserved hypot
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[illegible]

Query Match	100.00	Score 39	PR 2	Length 100
Best Local Similarity	100.00	Prod. No 2.3		
Matches	6	Conservative	0	Mismatches 0
				Total = 0
				Gaps 0

64 FIDMTD 69

RESULT 2
E69016

C:Accession: F69016

1. Baofeng 179 7195-7165 1997

A:Reference number: A69000; MUID:98037514
A:Accession: F69016

A. Residues - 1-348 MFE
A. Residues - 1-348 MFE

[illegible][illegible]

RECEIVED

superficially, *Caecorhabdus ciliaris* and *C. speciosus*.

Query Match: 84.8% Score 28, EB 2, Length 363,
Best Local Similarity: 84.8% Pred. No. 59;
Matches: 51 Conserved: 17 Mismatches: 0; Indels: 0; Gaps: 0;

QY 1 FEDMTD 4
11111
Db 57 FEDMTD 42

Result 15

S64082
Probably membrane protein (GDB). Yeast (Saccharomyces cerevisiae)

N:Alternate names: hypothetical protein G319

C:Species: Saccharomyces cerevisiae

C:Date: 17 May 1996 #seq_change_revision 17 May 1996 #text_change 14-Nov-1997

C:Accession: S64082

R:Rieger, M.; Mueller-Auer, S.; Bruckner, M.; Schaefer, M.
submitted to the Protein Sequence Database, May 1996

A:Reference number: S64071

A:Accession: S64082

A:Molecule type: DNA

A:Residues: 1387 (RIB)

A:Transmembrane: DMBL27597, NID432589, FTL243961, FLD432589, MFS, NID750

A:Experimental source: strain S286C

C:Genetics:

A:Map position: 7L

C:Keywords: transmembrane protein

F311277, GDB, 11 Nov 1996 #seq_change_revision 17 May 1996 #text_change 14-Nov-1997

Query Match: 94.8% Score 28, DB 2, Length 387;
Best Local Similarity: 83.3% Pred. No. 63;

Matches: 51 Conserved: 0; Mismatches: 17 Indels: 0; Gaps: 0;

QY 1 FEDMTD 4
11111
Db 361 FEDMTD 366

Search completed: June 22, 1999, 10:58:45
Job time: 14 sec




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AC      BAD4 YEAST          STANFORD.      EFTL      754 AA
AD      PLAT16:
DI      01-APR-1990 (REL. 14, CREATED)
DI      01-APR-1990 (REL. 14, LAST SEQUENCE UPDATE)
DI      01-NOV-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE      DNA REPAIR PROTEIN RAD4.
CN      PAR1 OF YEP162.
OS      SACCHAROMYCES CEREVISIAE (BAKE'S YEAST)
OC      EUCARYOTA EUK10 ARCHAEOTRITRIN ERMASCOMITRITS
EN      [1]
FP      SEQUENCE FROM N.A.
FX      MEDLINE: 2407274;
RA      GLEIF R.D., PAKASH S.A.
RL      GENE 711530 C11128991.
RN      121
RC      SEQUENCE FROM N.A.
RX      MEDLINE: 84197751.
RA      GLEIF R.D., FRIEDBERG E.C.
RL      BACTERIOL. 1711:1862-1864(1989).
RN      131
RC      SEQUENCE FROM N.A.
RA      WITTIGMAN I.T., DITTECH F.S., HENNESSEY K.M., SEHL P., KOMP C.,
RA      WITVIT TAVIR P., NAKAHARA K., FREDER D., DAVIS R.W.;
RL      SUBMITTED (FEB-1993) TO EMBL/GENBANK/DBPI DATA BANKS.
RN      141
RC      SEQUENCE FROM N.A.
RA      STEIN J.B., ARISTO.
RA      DITTECH F.S., WITTIGMAN I.T., HENNESSEY K.M., ALLEN E., APARTO F.P.,
RA      AILLES E., GERO A., BRENNAN T., CARPENTER J., CHEN E., CHERRY J.M.,
RA      CHONG F., GONAN M., GYAN F., HAPITZEL G., HINCKE-SMITH S.,
RA      HUMAN F., WATSEY A., KEMP G., LASHKAR D., LYN H., LIN D.,
RA      MORGENTHAU E., NAKAHARA K., NAMATH A., NORGREN P., OFFENBER P., OH C.,
RA      PETER F.X., ROBERTS D., SEHL P., SCHRAM S., SHOGREN I., SMITH V.,
RA      TAYLOR P., WEI Y., YELTON M., HIRSTEIN D., DAVIS R.W.;
RL      SUBMITTED (FEB-1994) TO EMBL/GENBANK/DBPI DATA BANKS.
CC      1. FUNCTION: INVOLVED IN MULTIPLE EXCISE-REPAIR OF DNA DAMAGED
CC      WITH UV LIGHT, HEAT, AGENTS, OR CROSS-LINKING AGENTS.
CC      2. SUBCELLULAR LOCATION: NUCLEAR.
CC      3. SIMILARITY: TO S-POMBE SPA-12H10 120 AND SOME, TO MAMMALIAN XPD.
CC      4. -1-
DR      EMBL: M21529: 3170251..
DR      EMBL: M21529: 3170251..
DR      EMBL: U18917: 5603402..
DR      PIR: S08742: D08924.
DR      PIR: S08742: D08924.
DR      PIR: S08081: J05081.
DR      PIR: S30814: S30814.
DR      SCD: L0601598: RAD4.
DR      SCD: L0601598: RAD4.
KW      DNA REPAIR; DNA-BINDING; NUCLEAR PROTEIN.
FT      DNA BIND 253..269
FT      CONFLICT 223..265
FT      CONFLICT 223..265
SC      SEQUENCE 754 AA: 5714 MW: 89556922 CRC32:
Query Match: 87.9% Score 291 DB 1: length 754;
Best Local Similarity: 83.3% Fnd No: 61.
Multiple: 1. Conservation: 1 Mismatch: 0. Models: 0. gaps
DY      1 EMBLID 5
DB      95 EMBLID 100

```

[illegible]

RC	STRAIN=168;
RA	FOULGER D., ERH

GenCorp version 4.5
Copyright (c) 1993 - 1998 CompuGen Ltd.

CM protein protein search, using sw model

Run on: June 22, 1999, 10:59:42 : Search time 45.16 seconds

(without alignments)
4.160 Million cell updates/sec

File: US-09-030-061-3

Perfect score: 3

Sequence: 1 EXLINX 7

Search: 1999-09-030-061-3

Database: SwissProt_35

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	100.0	193	1 IL18_HUMAN	Q14116 homo sapien
2	22	100.0	192	1 IL18_MOUSE	F31918 mus muscula
3	22	97.0	215	1 CYA_POTAN	Q01513 potamogeton
4	22	97.0	215	1 CYA_POTAN	Q01513 potamogeton
5	22	97.0	215	1 CYA_POTAN	Q01513 potamogeton
6	22	97.0	215	1 CYA_POTAN	Q01513 potamogeton
7	22	97.0	215	1 CYA_POTAN	Q01513 potamogeton
8	22	97.0	215	1 CYA_POTAN	Q01513 potamogeton
9	22	97.0	215	1 CYA_POTAN	Q01513 potamogeton
10	22	97.0	215	1 CYA_POTAN	Q01513 potamogeton
11	22	97.0	215	1 CYA_POTAN	Q01513 potamogeton
12	22	97.0	215	1 CYA_POTAN	Q01513 potamogeton
13	22	97.0	215	1 CYA_POTAN	Q01513 potamogeton
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15	22	97.0	215	1 CYA_POTAN	Q01513 potamogeton
16	22	97.0	215	1 CYA_POTAN	Q01513 potamogeton
17	22	97.0	215	1 CYA_POTAN	Q01513 potamogeton
18	22	97.0	215	1 CYA_POTAN	Q01513 potamogeton
19	22	97.0	215	1 CYA_POTAN	Q01513 potamogeton
20	22	97.0	215	1 CYA_POTAN	Q01513 potamogeton
21	22	97.0	215	1 CYA_POTAN	Q01513 potamogeton
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24	22	97.0	215	1 CYA_POTAN	Q01513 potamogeton
25	22	97.0	215	1 CYA_POTAN	Q01513 potamogeton
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28	22	97.0	215	1 CYA_POTAN	Q01513 potamogeton
29	22	97.0	215	1 CYA_POTAN	Q01513 potamogeton
30	22	97.0	215	1 CYA_POTAN	Q01513 potamogeton
31	22	97.0	215	1 CYA_POTAN	Q01513 potamogeton
32	22	97.0	215	1 CYA_POTAN	Q01513 potamogeton
33	22	97.0	215	1 CYA_POTAN	Q01513 potamogeton
34	22	97.0	215	1 CYA_POTAN	Q01513 potamogeton
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36	22	97.0	215	1 CYA_POTAN	Q01513 potamogeton
37	22	97.0	215	1 CYA_POTAN	Q01513 potamogeton
38	22	97.0	215	1 CYA_POTAN	Q01513 potamogeton
39	22	97.0	215	1 CYA_POTAN	Q01513 potamogeton
40	22	97.0	215	1 CYA_POTAN	Q01513 potamogeton
41	22	97.0	215	1 CYA_POTAN	Q01513 potamogeton
42	22	97.0	215	1 CYA_POTAN	Q01513 potamogeton
43	22	97.0	215	1 CYA_POTAN	Q01513 potamogeton

ALIGNMENTS

RESULT 1

ID IL18_HUMAN STANDARD: PRT: 193 AA.

AC Q14116:

DT 15-JUL-1998 (REL. 35) (CREATED)

DI 15-JUL-1998 (REL. 35) (LAST SEQUENCE UPDATE)

DI 15-JUL-1998 (REL. 35) (LAST ANNOTATION UPDATE)

DE INTERFERON-16 PREPROPEPTIDE (1-16) (INTERFERON-GAMMA INDUCING FACTOR)

DE (IFN-GAMMA INDUCING FACTOR) (INTERFERON-GAMMA) (IFN-GAMMA)

GN IL18 OR IGIF

OS HOMO SAPIENS (HUMAN)

OC ERYTHROCYTES, METASTASIS, CHLORATA, VERTEBRATA, TETRAPODA, MAMMALIA

OC ERYTHROCYTES, PRIMATES

OC ERYTHROCYTES, PRIMATES

OC ERYTHROCYTES, PRIMATES

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OC ERYTHROCYTES, PRIMATES

44 26 78.8 154 1 YVAR_BAUSG 14574 bacillus su

45 26 78.8 154 1 YVAR_BAUSG 14574 bacillus su

ALIGNMENTS

RESULT 2

ID IL18_MOUSE STANDARD: PRT: 193 AA.

AC Q14116:

DT 15-JUL-1998 (REL. 35) (CREATED)

DI 15-JUL-1998 (REL. 35) (LAST SEQUENCE UPDATE)

DI 15-JUL-1998 (REL. 35) (LAST ANNOTATION UPDATE)

DE INTERFERON-16 PREPROPEPTIDE (1-16) (INTERFERON-GAMMA INDUCING FACTOR)

DE (IFN-GAMMA INDUCING FACTOR) (INTERFERON-GAMMA) (IFN-GAMMA)

GN IL18 OR IGIF

OS HOMO SAPIENS (HUMAN)

OC ERYTHROCYTES, METASTASIS, CHLORATA, VERTEBRATA, TETRAPODA, MAMMALIA

OC ERYTHROCYTES, PRIMATES

OC ERYTHROCYTES, PRIMATES

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OC ERYTHROCYTES, PRIMATES

OC ERYTHROCYTES, PRIMATES


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1000  PAI
1001  TITL: RAT
1002  STANDARD:
1003  PRT: 416 AA
1004  1-1000
1005  1-1000 (PRT: 24, CREATED)
1006  1-1000 (PRT: 24, LAST SEQUENCE UPDATE)
1007  1-1000 (PRT: 24, LAST ANNOTATION UPDATE)
1008  TRANSCRIPTION INITIATION FACTOR IIB (TFIIB) (RNA POLYMERASE II
1009  ALPHA INITIATION FACTOR).
1010  TFIIB.
1011  RATIUS N-TERMINUS (RAI).
1012  PROTEIN: RATIUS N-TERMINUS, VERTEBRATA; TETRAPODA; MAMMALIA;
1013  RODENTIA; SCIENTIA.
1014  1-1000
1015  SEQUENCE: P M N A
1016  1-1000
1017  MILENE: 1-1000
1018  TITL: A
1019  TITL: K. P. CONWAY R. G. CONWAY J. W.
1020  NUCLEIC ACID: 21-42-4250(1992).
1021  1-1000
1022  FUNCTION: GENERAL FACTOR THAT PLAYS A MAJOR ROLE IN THE ACTIVATION
1023  OF EUKARYOTIC GENES TRANSCRIBED BY RNA POLYMERASE II.
1024  SUBUNIT ASSOCIATES WITH TFIID-11A (TAA COMPLEX) TO FORM TFIID-
1025  11A-TFIIB COMPLEX WHICH IS THEN RECOGNIZED BY POLYMERASE II.
1026  SUBC: TFIIB BELONGS TO THE TFIIB FAMILY
1027  1-1000
1028  EMBL: X6-42-1000
1029  EMBL: S26-42-1000
1030  TRANSFAC: 1-2100
1031  PROSITE: PS00742, TFIIB_2
1032  TRANSCRIPTION INITIATION, NUCLEAR PROTEIN, REPEAT, ZINC-FINGER,
1033  BINDING, 1-1000
1034  REF: 1-1000
1035  REF: 1-1000
1036  SEQUENCE: 1-1000
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1099  1-1000
1100  1-1000

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1000 TITL: RAT
 1001 STANDARD:
 1002 PRT: 416 AA
 1003 1-1000
 1004 1-1000 (PRT: 24, CREATED)
 1005 1-1000 (PRT: 24, LAST SEQUENCE UPDATE)
 1006 1-1000 (PRT: 24, LAST ANNOTATION UPDATE)
 1007 TRANSCRIPTION INITIATION FACTOR IIB (TFIIB) (RNA POLYMERASE II
 1008 ALPHA INITIATION FACTOR).
 1009 TFIIB.
 1010 RATIUS N-TERMINUS (RAI).
 1011 PROTEIN: RATIUS N-TERMINUS, VERTEBRATA; TETRAPODA; MAMMALIA;
 1012 RODENTIA; SCIENTIA.
 1013 1-1000
 1014 SEQUENCE: P M N A
 1015 1-1000
 1016 MILENE: 1-1000
 1017 TITL: A
 1018 TITL: K. P. CONWAY R. G. CONWAY J. W.
 1019 NUCLEIC ACID: 21-42-4250(1992).
 1020 1-1000
 1021 FUNCTION: GENERAL FACTOR THAT PLAYS A MAJOR ROLE IN THE ACTIVATION
 1022 OF EUKARYOTIC GENES TRANSCRIBED BY RNA POLYMERASE II.
 1023 SUBUNIT ASSOCIATES WITH TFIID-11A (TAA COMPLEX) TO FORM TFIID-
 1024 11A-TFIIB COMPLEX WHICH IS THEN RECOGNIZED BY POLYMERASE II.
 1025 SUBC: TFIIB BELONGS TO THE TFIIB FAMILY
 1026 1-1000
 1027 EMBL: X6-42-1000
 1028 EMBL: S26-42-1000
 1029 TRANSFAC: 1-2100
 1030 PROSITE: PS00742, TFIIB_2
 1031 TRANSCRIPTION INITIATION, NUCLEAR PROTEIN, REPEAT, ZINC-FINGER,
 1032 BINDING, 1-1000
 1033 REF: 1-1000
 1034 REF: 1-1000
 1035 SEQUENCE: 1-1000
 1036 1-1000
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 1100 1-1000

1000 TITL: RAT
 1001 STANDARD:
 1002 PRT: 416 AA
 1003 1-1000
 1004 1-1000 (PRT: 24, CREATED)
 1005 1-1000 (PRT: 24, LAST SEQUENCE UPDATE)
 1006 1-1000 (PRT: 24, LAST ANNOTATION UPDATE)
 1007 TRANSCRIPTION INITIATION FACTOR IIB (TFIIB) (RNA POLYMERASE II
 1008 ALPHA INITIATION FACTOR).
 1009 TFIIB.
 1010 RATIUS N-TERMINUS (RAI).
 1011 PROTEIN: RATIUS N-TERMINUS, VERTEBRATA; TETRAPODA; MAMMALIA;
 1012 RODENTIA; SCIENTIA.
 1013 1-1000
 1014 SEQUENCE: P M N A
 1015 1-1000
 1016 MILENE: 1-1000
 1017 TITL: A
 1018 TITL: K. P. CONWAY R. G. CONWAY J. W.
 1019 NUCLEIC ACID: 21-42-4250(1992).
 1020 1-1000
 1021 FUNCTION: GENERAL FACTOR THAT PLAYS A MAJOR ROLE IN THE ACTIVATION
 1022 OF EUKARYOTIC GENES TRANSCRIBED BY RNA POLYMERASE II.
 1023 SUBUNIT ASSOCIATES WITH TFIID-11A (TAA COMPLEX) TO FORM TFIID-
 1024 11A-TFIIB COMPLEX WHICH IS THEN RECOGNIZED BY POLYMERASE II.
 1025 SUBC: TFIIB BELONGS TO THE TFIIB FAMILY
 1026 1-1000
 1027 EMBL: X6-42-1000
 1028 EMBL: S26-42-1000
 1029 TRANSFAC: 1-2100
 1030 PROSITE: PS00742, TFIIB_2
 1031 TRANSCRIPTION INITIATION, NUCLEAR PROTEIN, REPEAT, ZINC-FINGER,
 1032 BINDING, 1-1000
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PR 25-FEB-1997; JP-055468.
 PA (HAYR) HAYASHIBARA SEIICHIRO KAGAKU
 PI Gillespie M, Harwood NJ, Kunitomo M, Udagawa N
 DP WPI: 98-44864/39.
 DR N-PSDB: V19226.
 QY Use of Interleukin-18 to inhibit osteoclast formation - in treatment
 PI of e.g. hypercalcaemia, osteoclastoma, Behcet's syndrome.
 PI osteoclastoma, chronic rheumatoid arthritis, deformity osteitis,
 PI primary hyperthyroidism and osteoporosis
 PS Claim 4: Page 18; 56pp; English.
 CC Interleukin-18 (IL-18) is a functional equivalent can be used for
 CC inhibition of osteoclast formation. IL-18 is used for treating or
 CC preventing osteoclast-related diseases e.g. hypercalcaemia, osteoclastoma
 CC Behcet's syndrome, osteoclastoma, arthropathy, chronic rheumatoid
 CC arthritis, deformity osteitis, primary hyperthyroidism, osteoporosis and
 CC osteoporosis.
 SO Sequence 157 AA;

Query Match 100.0% Score 816; DB 1; Length 157.
 Best Local Similarity 100.0%; Pred. No. 4.7e-83;
 Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFVKLSKLVNFKVNFVLTGKPNFMKTSKPNAPFIFISWYISQPHKM 10
 DB 1 YFVKLSKLVNFKVNFVLTGKPNFMKTSKPNAPFIFISWYISQPHKM 10
 QY 51 AVIISVGVSVNFKVNFVLTGKPNFMKTSKPNAPFIFISWYISQPHKM 120
 DB 61 AVIISVGVSVNFKVNFVLTGKPNFMKTSKPNAPFIFISWYISQPHKM 120
 QY 121 EGYFLAGEKPEFLKILKKEDELGDSIMFTVONED 157
 DB 121 EGYFLAGEKPEFLKILKKEDELGDSIMFTVONED 157

RESULT 5
 W77082
 ID W77082 standard protein 193 AA.

DE Interleukin 18 active protein and precursor
 KW Human Interleukin-18; IL-18; osteoclast; hypercalcaemia; osteopenia;
 KW osteoclastoma; Behcet's syndrome; osteoclastoma; arthropathy; osteoporosis;
 KW chronic rheumatoid arthritis; deformity osteitis; primary hyperthyroidism;
 OS Homo sapiens.

PI Key location/qualifiers
 PI Peptide 1-136
 PI Peptide /note "Signal peptide"
 PI 47-193

PI EP-91562-AE.
 PD 25-SEP-1998.
 PE 25-SEP-1998; 05:05:00.
 PA 25-FEB-1997; JP-055468.
 PI (HAYR) HAYASHIBARA SEIICHIRO KAGAKU
 PI Gillespie M, Harwood NJ, Kunitomo M, Udagawa N
 DP WPI: 98-44864/39.
 DR N-PSDB: V4828.

PI Use of Interleukin-18 to inhibit osteoclast formation - in treatment
 PI of e.g. hypercalcaemia, osteoclastoma, Behcet's syndrome,
 PI osteoclastoma, chronic rheumatoid arthritis, deformity osteitis,
 PI primary hyperthyroidism and osteoporosis

PS Interleukin-18 (IL-18) is a functional equivalent can be used for
 CC inhibition of osteoclast formation. IL-18 is used for treating or
 CC preventing osteoclast-related diseases e.g. hypercalcaemia, osteoclastoma
 CC Behcet's syndrome, osteoclastoma, arthropathy, chronic rheumatoid
 CC arthritis, deformity osteitis, primary hyperthyroidism, osteopenia and
 CC osteoporosis.
 SO Sequence 193 AA;

Query Match 99.4% Score 813; DB 1; Length 193.
 Best Local Similarity 99.4%; Pred. No. 1.3e-83;
 Matches 157; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 YFVKLSKLVNFKVNFVLTGKPNFMKTSKPNAPFIFISWYISQPHKM 50
 DB 37 YFVKLSKLVNFKVNFVLTGKPNFMKTSKPNAPFIFISWYISQPHKM 56
 QY 61 AVIISVGVSVNFKVNFVLTGKPNFMKTSKPNAPFIFISWYISQPHKM 120
 DB 61 AVIISVGVSVNFKVNFVLTGKPNFMKTSKPNAPFIFISWYISQPHKM 120
 QY 121 EGYFLAGEKPEFLKILKKEDELGDSIMFTVONED 157
 DB 121 EGYFLAGEKPEFLKILKKEDELGDSIMFTVONED 157

RESULT 6
 R99564
 ID R99564 standard protein 157 AA.

DE Human Interferon-gamma inducer protein.
 KW Interferon gamma inducer protein; IFN-gamma; antiviral; virucide;
 KW antitumor; antibacterial; immunoregulator; adoptive immunotherapy;
 KW therapy; cancer.
 OS Homo sapiens.

PI Key location/qualifiers
 PI misc-difference 73
 PI /label= Ile, Thr
 PI EP-712931-A2.
 PD 22-MAY-1996.
 PE 10-NOV-1995; 40805.
 PA 15-NOV-1994; JP-058240.
 PR 23-FEB-1995; JP-078357.
 PR 10-MAR-1995; JP-078357.
 PR 18-SEP-1995; JP-062062.
 PR 29-SEP-1995; JP-274988.
 PA (HAYR) HAYASHIBARA SEIICHIRO KAGAKU
 PI Fukuda S, Kohno K, Kunitomo M, Kunitomo M, Okamura H
 PI Taniguchi M, Tanimoto T, Torioka K, Ushio S
 DP WPI: 98-25837/26.
 DR N-PSDB: T32411.
 PI CNA encoding Interferon-gamma protein, including polypeptide - useful
 PI to treat and prevent, e.g. viral disease, malignancies and immune
 PI disorders
 PS Example P-1-1: Page 28; 48pp; English.
 CC A novel human protein (R99564) that induces interferon-gamma
 CC (IFN-gamma) production by immunocompetent cells is the product of a
 CC phage cDNA clone (T32411) derived from a human liver library.
 CC PCR amplification of the cDNA (see also T32409-10) and expression
 CC in Escherichia coli. Xu L Blue MarKan allowed production of recombinant
 CC induced protein. This was used to construct hybridoma H-1, which
 CC produced anti-IFN-gamma inducer protein monoclonal antibody H-1mAb,
 CC useful in the detection and purification of the inducer protein
 CC (see also R99558).
 SO Sequence 157 AA;

Query Match 99.4% Score 811; DB 1; Length 157.
 Best Local Similarity 99.4%; Pred. No. 1.7e-83;
 Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YFVKLSKLVNFKVNFVLTGKPNFMKTSKPNAPFIFISWYISQPHKM 50
 DB 1 YFVKLSKLVNFKVNFVLTGKPNFMKTSKPNAPFIFISWYISQPHKM 50
 QY 61 AVIISVGVSVNFKVNFVLTGKPNFMKTSKPNAPFIFISWYISQPHKM 120
 DB 61 AVIISVGVSVNFKVNFVLTGKPNFMKTSKPNAPFIFISWYISQPHKM 120
 QY 121 EGYFLAGEKPEFLKILKKEDELGDSIMFTVONED 157
 DB 121 EGYFLAGEKPEFLKILKKEDELGDSIMFTVONED 157


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SU Sequence 157 AA:
Query Match/b      99.4% Score 811: DB 1: Length 157:
Host Local Similarity 99.4% Pred No.1.7e-82:
Matches 166: Conservative 0: Mismatches 1: Indels 0: Gaps
          1 YFKRSKSLVFNPNMSEVFITGQNPPIEFMTSTGCPNAPRTFTISWYRSLTQM 60
          1 IFFRKSRSTSVENPNEVFIFGNGEPFIPEPTTSCTPPNAFTFTISWYRSGPRFM 60
DB   61 AVTISVCVCVTSSCEWTISEWVEVPENINIKLSQILFQAGVGVGNVGMVMSSESY 120
        AATTISKCRISXLSLTFNKITSFEMKPDPNNIKNTSGLIIPDQSVPHNPKWPSSEST 120
          121 EGYFLATREPGQLLELLMLKEDEEDSPSIMVEDND 157
          121 EYFLATREPGQLLELLMLKEDEEDSPSIMVEDND 157
RESULT 11
W47429
W47429 standard; Protein; 193 AA.
AC W47429:
DT 05-JUN-1998 (first entry)
DE Interferon-gamma production inducer.
KW Interferon gamma, IFN-gamma; production inducer; gene therapy;
KW immunocompetent cells; treatment; prevention; malignant tumour;
KW viral infection; bacterial infection; immune disease.
OS Homo sapiens.
FH Key
FT Peptide
    Location/Qualifiers
    1..36
    FT Peptide
        /label=seq-peptide
    37..109
    FT Peptide
        /label=mcl-peptide
    109
    FT Misc-difference
        /label= 1le, Thr
    F1
    F1
    F1 EP-816499-A2.
    PN
    PD 07-JAN-1998.
    PF 27-JUN-1997: 304616
    PE 27-JUN-1996: JP-185305.
    PA (HAYB ) HAYASHIBARA SEIBUTSU KAKAKU.
    PI Katsumoto M, Okada T, Terakado K;
    ID W47429:414706.
    DR N-PDB: W15825, W15826.
    PT Genomic DNA encoding polypeptide inducing interferon-gamma
    P1 production - by immuno-competent cells, useful to treat e.g. human
    P1 malignant tumours or viral diseases
    PS Claim 2: Pages 49-50; 74pp; English.
    CC The present sequence is a protein, which induces
    CC interleukin gamma (IFN-gamma) production in immunocompetent cells.
    CC The protein has high biological activity, including enhancing
    CC cytotoxicity of killer cells and inducing killer cell formation,
    CC In addition to inducing IFN-gamma production by immunocompetent
    CC cells when expressed in mammalian cells, facilitating its use in
    CC low dosages by oral/intravit. e.g. malignant tumours, viral or
    CC bacterial infections and immune diseases. As it is expressed in
    CC mammalian cells, it also has low toxicity when used in human
    CC treatments, maintaining side effects. The DNA encoding the protein
    CC can be used in gene therapy, e.g. by injecting vectors containing
    CC the DNA or transplanting cells.
    SO Sequence 193 AA.
Query Match      99.4% Score 811: DB 1: Length 193:
Host Local Similarity 99.4% Pred. No.2.2e 82:
Matches 166: Conservative 0: Mismatches 1: Indels 0: Gaps
          1 YFKRSKSLVFNPNMSEVFITGQNPPIEFMTSTGCPNAPRTFTISWYRSLTQM 60
          1 IFFRKSRSTSVENPNEVFIFGNGEPFIPEPTTSCTPPNAFTFTISWYRSGPRFM 60
DB   37 AVTISVCVCVTSSCEWTISEWVEVPENINIKLSQILFQAGVGVGNVGMVMSSESY 120
        AATTISKCRISXLSLTFNKITSFEMKPDPNNIKNTSGLIIPDQSVPHNPKWPSSEST 120
          121 EGYFLATREPGQLLELLMLKEDEEDSPSIMVEDND 157
          121 EYFLATREPGQLLELLMLKEDEEDSPSIMVEDND 157

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11
 12 AV: VPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 156
 13
 14 EGI: VAVKPKKAKKAKKEDNRSMPVQNTD 157
 15
 16 EGI: VAVKPKKAKKAKKEDNRSMPVQNTD 157
 17
 18 EGI: VAVKPKKAKKAKKEDNRSMPVQNTD 157
 19
 20 EGI: VAVKPKKAKKAKKEDNRSMPVQNTD 157
 21
 22 EGI: VAVKPKKAKKAKKEDNRSMPVQNTD 157
 23
 24 EGI: VAVKPKKAKKAKKEDNRSMPVQNTD 157
 25
 26 EGI: VAVKPKKAKKAKKEDNRSMPVQNTD 157
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 28 EGI: VAVKPKKAKKAKKEDNRSMPVQNTD 157
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 30 EGI: VAVKPKKAKKAKKEDNRSMPVQNTD 157
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 90 EGI: VAVKPKKAKKAKKEDNRSMPVQNTD 157
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 92 EGI: VAVKPKKAKKAKKEDNRSMPVQNTD 157
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 94 EGI: VAVKPKKAKKAKKEDNRSMPVQNTD 157
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 98 EGI: VAVKPKKAKKAKKEDNRSMPVQNTD 157
 99
 100 EGI: VAVKPKKAKKAKKEDNRSMPVQNTD 157

18-JUL-1997: 305377.
 19-MAY-1997: 3055002.
 19-JUL-1996: JP-207691.
 PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
 PI Kurimoto M, Tanimoto T.
 DR WFI: 98-078818/08.
 DR N-PSDB: V17200.
 PT Polypeptide-processing enzyme - for preparing mature form of
 PT interferon-inducing polypeptide
 PS Claim 3: Page 15: 18pp: English.
 CC This sequence represents the precursor of an interferon gamma (IFN-gamma)
 CC inducing polypeptide. The polypeptide induces IFN-gamma production in
 CC immunocompetent cells (the polypeptide is not named but is described in
 CC JP 27198/96 and JP 27199/96). An enzyme can convert this precursor form
 CC into its active form by cleaving a linkage between Asp at amino acid
 CC position 36 and Tyr at amino acid position 37 of its N-terminal flanking
 CC. The enzyme can be obtained from a human haematopoietic cell and can be
 CC inhibited by iodoacetamide and acetyl-L-tyrosyl-L-valyl-L-alanyl-L-aspart
 CC -1-91. The enzyme can be used for cleaving a recombinant IFN-gamma
 CC pro polypeptide to form a mature polypeptide.
 CC Sequence 193 AA:
 SO
 Query Match 99.4% Score 811 DB 1: Length 194
 Best local similarity 99.4% Prod No: 2,29-84
 Matches 156 Conservative 0 Mismatches 1 Indels 0 Gaps 0
 1 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 2 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 3 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 4 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 5 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 6 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
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 8 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
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 11 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 12 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 13 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 14 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 15 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 16 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
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 21 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
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 33 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 34 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 35 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 36 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 37 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 38 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 39 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 40 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 41 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 42 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 43 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 44 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 45 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 46 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 47 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 48 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 49 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 50 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 51 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 52 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 53 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 54 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 55 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 56 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 57 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 58 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 59 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 60 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 61 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 62 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 63 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 64 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 65 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 66 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 67 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 68 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 69 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 70 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 71 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 72 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 73 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 74 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 75 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
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 77 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
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 80 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 81 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 82 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 83 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 84 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 85 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 86 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 87 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 88 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 89 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 90 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 91 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 92 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 93 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 94 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 95 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 96 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 97 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 98 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 99 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157
 100 YPEKFSKISVNIINNGVIFINQNPPIPTMTISQVFNQVSPHNMVLFSSSY 157



1	8.44	100.0	180	1	W4960	Wild-type mouse-1
2	8.44	100.0	157	1	W7078	Mouse interleukin
3	8.04	99.3	157	1	W6559	Interferon gamma
4	8.04	99.3	157	1	W6559	Mouse mature info
5	8.04	99.3	157	1	W5704	Mouse interferon- γ
6	8.04	99.3	157	1	W5704	Mouse interferon- γ
7	8.04	99.3	157	1	W5704	Mouse IL-18 prote
8	8.04	99.3	157	1	W5704	Mouse interleukin
9	8.04	99.3	157	1	W4968	Mutant mouse inte
10	8.04	99.3	157	1	W7078	Mouse interleukin
11	8.04	99.3	157	1	W4969	Mutant mouse inte
12	8.04	99.3	157	1	W7091	Mouse interleukin
13	8.04	99.3	157	1	W7091	Mouse interleukin
14	8.04	99.3	157	1	W7091	Mouse interleukin
15	8.04	99.3	157	1	W7091	Mouse interleukin
16	8.04	99.3	157	1	W7091	Mouse interleukin
17	8.04	99.3	157	1	W7091	Mouse interleukin
18	8.04	99.3	157	1	W7091	Mouse interleukin
19	8.04	99.3	157	1	W7091	Mouse interleukin
20	8.04	99.3	157	1	W7091	Mouse interleukin
21	8.04	99.3	157	1	W7091	Mouse interleukin
22	8.04	99.3	157	1	W7091	Mouse interleukin
23	8.04	99.3	157	1	W7091	Mouse interleukin
24	8.04	99.3	157	1	W7091	Mouse interleukin
25	8.04	99.3	157	1	W7091	Mouse interleukin
26	8.04	99.3	157	1	W7091	Mouse interleukin
27	8.04	99.3	157	1	W7091	Mouse interleukin
28	8.04	99.3	157	1	W7091	Mouse interleukin
29	8.04	99.3	157	1	W7091	Mouse interleukin
30	8.04	99.3	157	1	W7091	Mouse interleukin
31	8.04	99.3	157	1	W7091	Mouse interleukin
32	8.04	99.3	157	1	W7091	Mouse interleukin
33	8.04	99.3	157	1	W7091	Mouse interleukin
34	8.04	99.3	157	1	W7091	Mouse interleukin
35	8.04	99.3	157	1	W7091	Mouse interleukin
36	8.04	99.3	157	1	W7091	Mouse interleukin
37	8.04	99.3	157	1	W7091	Mouse interleukin
38	8.04	99.3	157	1	W7091	Mouse interleukin
39	8.04	99.3	157	1	W7091	Mouse interleukin
40	8.04	99.3	157	1	W7091	Mouse interleukin
41	8.04	99.3	157	1	W7091	Mouse interleukin
42	8.04	99.3	157	1	W7091	Mouse interleukin

PR 14-NOV-1997; JP-329715.
PR 29-NOV-1996; JP-333037.

PR 21-JAN-1997, JP-024908.
PA (HAYR.) HAYASHIBARA SHIGETSU KAGAWA.
P1 Kurimoto M., Okamoto T., Yamamoto K.
25 REF: 38-0287-72-76.
26
27 N-PSD; V32755.
28
29 Mutants of interferon gamma inducing polypeptides useful as
P1 antitumor, antiviral, antimicrobial or anti immunophable agents
P2 Claim 4, pages 38-39, 59pp. English.
30 The present sequence represents the wild-type mouse interferon gamma
31 inducing factor (mIGIF). The invention provides for mutant human and
32 mouse interferon gamma inducing factors in which one or more cysteine
33 residues are replaced with different residues at or away from the
34 consensus sequence shown in W49696-W4998. The mutant mIGIFs are
35 capable of stimulating the development of cells for the treatment of
36 interferon gamma and are claimed to be less toxic, more active and stable
37 than the corresponding wild type mIGIF. The mutant mIGIFs are also
38 claimed to enhance killing of cell cytotoxicity and/or induce killer cell
39 formation, and may therefore be useful as antitumor agents, antitumor
40 immunomodulatory, antiviral agents and antimicrobial agents. The
41 mutant mIGIFs are also claimed to be useful for treating hepatitis,
42 acquired immunodeficiency syndrome (AIDS), malaria, leishmaniasis, solid
43 malignant tumours (e.g. renal carcinoma), rheumatism, osteoporosis and
44 immunodeficiency caused by radiation and chemotherapy.
45 Sequence 180 AA.

Query Match	100.00	Score 612	DB 1	Length 187
Best Local Similarity	100.00	Pred. No. 4, 10-77		
Matches 100	Conservative	Mismatches	0	Indels 0

05	123	HEIADCEBFAKKTTPVPEENELR	SYMPILIN	HAS	157
06					
144	144	HEIADCEBFAKKTTPVPEENELR	SYMPILIN	HAS	180

RESULT 2

CC Carrying the GNA.
SO Sequence 157 AA

Query Match 99.3% Score 806 DB 1 Length 157
Best Local Similarity 99.4% Prod No 14e-76
Matches 156 Conservative 0 Mismatches 1 Indels 0 Gaps 0

0Y 1 NPSRLHCTIVAVININNOVIFVKRPQVPEFMDIDQASAPSPQRLIIMYKDSVEVGLA 60
DB 1 NPSRLHCTIVAVININNOVIFVKRPQVPEFMDIDQASAPSPQRLIIMYKDSVEVGLA 60
0Y 61 VITLVAVTSMSTISCKNRTISFEEMKPEPNIDQISLLEFQKVPVGNKKMEFESSLEYG 120
DB 61 VITLVAVTSMSTISCKNRTISFEEMKPEPNIDQISLLEFQKVPVGNKKMEFESSLEYG 120
0Y 121 HFLACQKEDJAFKLLIKKDKGKSVMTITLNHQS 157
DB 121 HFLACQKEDJAFKLLIKKDKGKSVMTITLNHQS 157

RESULT 5

W63812
ID W63812 standard; protein; 157 AA.
AC W63812
DE 15-OCT-1997 (first entry)
DT Mouse protein for induction of interferon-gamma.
KW Interferon-gamma, immunocompetent cells, malignant tumour;
KW viral disease; bacterial infection; immune disease.
OS Mus musculus.
FI misc-difference 70 Location/Qualifiers
FT J09157180-A.
PN 17-FEB-1997
PR 24-SEP-1998 JP-269105
PR 24-SEP-1998 JP-269105
PR 26-SEP-1995 JP-270725
PR 26-SEP-1995 JP-270725
PA (HAYE) HAYASHIBARA SEIROUO KASAKU.
PI Akita K, Fujii M, Kurimoto M, Nukada Y, Tanimoto T.
DR N-PSDB: T60536.
PI Human protein that induces interferon-gamma prodn. in
PI immune competent cells - useful for adoptive immunotherapy of
PI tumours and as antimicrobial agent etc.
PS Discourse: Page 22, 25pp, English.
CC The present sequence represents a novel protein from mouse liver cells,
CC which induces interferon-gamma (IFN gamma) production in immunocompetent
CC cells. This protein enhances cytotoxicity of killer cells and induces
CC their formation. It is used as an antineoplastic agent for antitumour
CC immunotherapy in animal (including anti-AIDS) or antitubercular agent,
CC and in the treatment of atopic or immune system diseases, e.g. asthma,
CC hay fever or rheumatism. When formulated with interleukin-3, it is also
CC used to treat leukaemia and thrombocytopenia associated with
CC cytotoxicity of chemotherapy of leukaemia and other cancers. When used
CC in antitumour immunotherapy, this novel protein significantly improves
CC the immunotherapeutic effect of interleukin-2 (IL-2) compared with the
CC administration of IL-2 or by addition to the medium in which cells
CC (harvested for return to the patient) are being grown.
SO Sequence 157 AA

Query Match 99.3% Score 806 DB 1 Length 157
Best Local Similarity 99.4% Prod No 14e-76
Matches 156 Conservative 0 Mismatches 1 Indels 0 Gaps 0

0Y 1 NPSRLHCTIVAVININNOVIFVKRPQVPEFMDIDQASAPSPQRLIIMYKDSVEVGLA 60
DB 1 NPSRLHCTIVAVININNOVIFVKRPQVPEFMDIDQASAPSPQRLIIMYKDSVEVGLA 60
0Y 61 VITLVAVTSMSTISCKNRTISFEEMKPEPNIDQISLLEFQKVPVGNKKMEFESSLEYG 120
DB 61 VITLVAVTSMSTISCKNRTISFEEMKPEPNIDQISLLEFQKVPVGNKKMEFESSLEYG 120
0Y 121 HFLACQKEDJAFKLLIKKDKGKSVMTITLNHQS 157
DB 121 HFLACQKEDJAFKLLIKKDKGKSVMTITLNHQS 157

RESULT 5
W15704

ID W15704 standard; peptide; 157 AA.

AC W15704

DT 26-JAN-1998 (first entry)

DE Mouse interferon-gamma inducer protein.

KW Interferon-gamma, IFN-gamma; antiviral; antineoplastic; radiotherapy;

KW immunoregulatory; antitumour agent; chemotherapy; leukaemia;

KW thymolymphoid; immunocompetent cells; asthma; hay fever;

KW rheumatism; interleukin; killer cell.

OS Mus musculus.

FI misc-difference 70 Location/Qualifiers

FT EF-767178-A1.
PN 09-APR-1997.
PR 24-SEP-1998 JP-269105.
PR 26-SEP-1995 JP-270725.
PR 26-SEP-1995 JP-270725.
PA (HAYE) HAYASHIBARA SEIROUO KASAKU.
PI Akita K, Fujii M, Kurimoto M, Nukada Y, Tanimoto T.
DR N-PSDB: T60536.
PI Human protein that induces interferon-gamma prodn. in
PI immune competent cells - useful for adoptive immunotherapy of
PI tumours and as antimicrobial agent etc.
PS Discourse: Page 22, 25pp, English.
CC The present sequence represents a novel protein from mouse liver cells,
CC which induces interferon-gamma (IFN gamma) production in immunocompetent
CC cells. This protein enhances cytotoxicity of killer cells and induces
CC their formation. It is used as an antineoplastic agent for antitumour
CC immunotherapy in animal (including anti-AIDS) or antitubercular agent,
CC and in the treatment of atopic or immune system diseases, e.g. asthma,
CC hay fever or rheumatism. When formulated with interleukin-3, it is also
CC used to treat leukaemia and thrombocytopenia associated with
CC cytotoxicity of chemotherapy of leukaemia and other cancers. When used
CC in antitumour immunotherapy, this novel protein significantly improves
CC the immunotherapeutic effect of interleukin-2 (IL-2) compared with the
CC administration of IL-2 or by addition to the medium in which cells
CC (harvested for return to the patient) are being grown.
SO Sequence 157 AA

Query Match 99.4% Score 806 DB 1 Length 157
Best Local Similarity 99.4% Prod No 14e-76
Matches 156 Conservative 0 Mismatches 1 Indels 0 Gaps 0

0Y 1 NPSRLHCTIVAVININNOVIFVKRPQVPEFMDIDQASAPSPQRLIIMYKDSVEVGLA 60
DB 1 NPSRLHCTIVAVININNOVIFVKRPQVPEFMDIDQASAPSPQRLIIMYKDSVEVGLA 60
0Y 61 VITLVAVTSMSTISCKNRTISFEEMKPEPNIDQISLLEFQKVPVGNKKMEFESSLEYG 120
DB 61 VITLVAVTSMSTISCKNRTISFEEMKPEPNIDQISLLEFQKVPVGNKKMEFESSLEYG 120
0Y 121 HFLACQKEDJAFKLLIKKDKGKSVMTITLNHQS 157
DB 121 HFLACQKEDJAFKLLIKKDKGKSVMTITLNHQS 157

RESULT 7
W63811

ID W63811 standard; protein; 157 AA.

AC W63811

DT 28-SEP-1998 (first entry)

DE Mouse IL-18 protein fragment.

KW Interleukin-18; IL-18; murine; treatment; autoimmune disease; antibody;

KW immunosuppressant; inhibitor; receptor protein; detection.

OS Mus sp.

FI key

FT Location/Qualifiers
FT 1..157
FT /label= IL-18
FT /note= "partial sequence"

DB 138 GHFLACGCKEDPAKFLVLRKXNDGCKSVMTLLNLKQS 175

RESULT 15

ID W48962 standard: Peptide: 157 AA.

AC W48962:

DI 25-SEP-1998 (first entry)

DE Mutant human interferon gamma inducing factor IGIF/MOT21.

KW Interferon-gamma inducing factor, Interferon-gamma, Killer cell,

KW Interferon-gamma inducing factor, antimicrobial agent; tumour; IGIF;

KW hepatitis; malaria; tuberculosis; renal carcinoma; rheumatism; AIDS;

KW osteoporosis, thrombocytosis, acquired immunodeficiency syndrome.

OS Homo sapiens.

OS Synthetic.

EH Key Location/Qualifiers

FI MISC_difference 38

FI /note= "changed from Cys in wild-type to Ser in mutant"

FI EP-845530-A2.

PN 03-JUN-1998.

PP 20-NOV-1998: 306622.

PR 14-NOV-1997: CP-329715.

PR 29-NOV-1996: CP-330037.

PP 21-JAN-1997: CP-020906.

PA (HAYB.) HAYASHIGARA SEIBUITSU KAGAKU.

PI KURIMOTO M OKAMOTO I, Yamamoto K;

DR WPI: 98-286147/25.

DR N-PSDB: V32626.

PI Mutants of interferon-gamma inducing polypeptide - useful as

PI antitumor, antiviral, antimicrobial or anti immunopathic agents

PS Claim 5: page 41: 59pp: English.

CC The present sequence represents the mutant human interferon-gamma

CC inducing factor IGIF/MOT21. The wild-type human interferon-gamma

CC factor sequence is shown in W48959. The invention provides for mutant

CC human and mouse interferon-gamma inducing factors (IGIF) in which one or

CC more cysteine residues are replaced with different residues at or away

CC from the consensus sequences shown in W48956-W48958. The mutant IGIFs

CC are capable of stimulating immunocompetent cells for the production of

CC interferon-gamma and are claimed to be less toxic, more active and

CC stable than the corresponding wild type interferon-gamma inducing

CC factor. The mutant IGIFs are also claimed to enhance killer cell

CC cytotoxicity and/or induce killer cell formation, and may therefore

CC be useful as antitumor agents, antitumor immunotherapeutics, antiviral

CC agents and antimicrobial agents. The mutant IGIFs are also claimed

CC to be useful for treating hepatitis, acquired immunodeficiency syndrome

CC (AIDS), malaria, tuberculosis, solid malignant tumours (e.g. renal

CC carcinoma), rheumatism, osteoporosis and thrombocytopenia caused by

CC radiation and chemo-therapy.

SO Sequence: 157 AA;

Query Match 64.8%, Score 526, DB 1, Length 157,

Best Local Similarity 65.6%; Pwd. No. 1.7e-47;

Matches 191; Conserved: 21; Mismatches 21; Indels 2; Gaps 2;

Q3 2 EGRHCTAVININQVIVFK-EGVFEEDMDITGSASEPTRLIYMYKSEVGLA 60

DB 2 PPTFSTKAVININQVIFEGNPTTHQMTQSSQMAAFITLISMKDSQPRGA 61

QY 61 VILSVKSKMSTISQNKSTISFEEMUPENIDIDSLDFEKKVPVGH-NKMEFESSLYE 119

DB 62 VTIIVKEFKISTISCEKSTISFEKMNPNIPKIDSLDFEESVYGHDKKQFPSSSYE 121

Q3 123 GYPLAAGCKEDPAKFLVLRKXNDGCKSVMTLLNLKQS 153

DB 122 GYPLACKEKEDPAKFLVLRKXNDGCKSVMTLLNLKQS 155

Search completed: June 22, 1999, 10:56:40
Job time: 79 sec



GenCore version 4.5
Copyright 1993-1998 Amgen Inc.

OM protein - protein search, using SW model

Run on: June 22, 1999, 10:55:21 : Search time 61.72 seconds

(without alignments)
1.666 Million cell updates/sec

Title: US-09-030-061-1

Perfect score: 31

Sequence: 1 NDVLF 6

Scoring table: PROSUM62

Search: 11879 893 202728 residues

Database: A_Geneseq_34:*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	100.0	157	1	Interferon gamma F
2	31	100.0	157	1	Human interferon-g
3	31	100.0	157	1	Human mature inter
4	31	100.0	157	1	Mouse mature inter
5	31	100.0	157	1	Human interferon-g
6	31	100.0	157	1	Human interferon-g
7	31	100.0	157	1	Human protein for
8	31	100.0	157	1	Interferon gamma 1
9	31	100.0	157	1	Interferon gamma 1
10	31	100.0	157	1	Interferon gamma 1
11	31	100.0	157	1	Mouse interferon-g
12	31	100.0	157	1	N-terminal fragment
13	31	100.0	157	1	Interferon gamma 1
14	31	100.0	157	1	Amino acid sequenc
15	31	100.0	157	1	Interferon gamma p
16	31	100.0	157	1	Interferon gamma 1
17	31	100.0	157	1	Interferon gamma 1
18	31	100.0	157	1	IFN-gamma inducing
19	31	100.0	157	1	Interferon gamma 1
20	31	100.0	157	1	Actin acid sequenc
21	31	100.0	157	1	Amino acid sequenc
22	31	100.0	157	1	Wild-type human in
23	31	100.0	157	1	Wild-type mouse in
24	31	100.0	157	1	Consensus sequence
25	31	100.0	157	1	Mutant human inter
26	31	100.0	157	1	Mutant human inter
27	31	100.0	157	1	Mutant human inter
28	31	100.0	157	1	Mutant human inter
29	31	100.0	157	1	Mutant human inter
30	31	100.0	157	1	Mutant human inter
31	31	100.0	157	1	Mutant mouse inter
32	31	100.0	157	1	Mutant mouse inter
33	31	100.0	157	1	Mutant mouse inter
34	31	100.0	157	1	Human IL-18 protei
35	31	100.0	157	1	Human interleukin
36	31	100.0	157	1	Human interleukin
37	31	100.0	157	1	Human interleukin
38	31	100.0	157	1	Human interleukin
39	31	100.0	157	1	Human interleukin
40	31	100.0	157	1	Human interleukin
41	31	100.0	157	1	Human interleukin
42	31	100.0	157	1	Human interleukin
43	31	100.0	157	1	Human interleukin

44 31 100.0 157 1 W77087 Human Interleukin
45 31 100.0 157 1 W77088 Human Interleukin

ALIGNMENTS

RESULT 1
R92506
ID R92506 standard: Protein, 157 AA.
AC R92506;
DE 02-SEP-1996 (first entry)
DE Interferon gamma production inducer protein.
KW Interferon gamma inducer IFNgamma, Imm, cytokine, cell, activator,
KW antitumor, antiseptic, immunoregulatory, platelet increasing agent,
KW theophylline, sodium acetate, renal cancer, brain cancer,
KW 910-1504, myeloid leukemia, rheumatism, allergy, cytokine, AIDS,
KW Interleukin, interleukin, IL-18, tumor necrosis factor (TNF),
KW adoptive immunotherapy, monoclonal antibody.
OS Mus musculus.
FH key Location/Qualifiers
FI misc_difference /0
HI /label= Met, Thr
LN E1-59-535-A2.
PD 17-JAN-1996.
PR 13-JUL-1995: 304906.
PR 14-JUL-1994: JP-184152.
PR 10-FEB-1995: JP-045057.
FA (HMB) HAYASHIBARA SEIHOUICHI KASAKI.
PI Kohno K, Kunikida T, Kurimoto M, Okamura H, Taniguchi M,
PI Tanimoto T, Toriige K;
PI WPI: 96-070177/08.
NP N-PSDB: R92506.
BT
PI Protein that induces gamma interferon prodn. in immunocompetent
PI cells - used e.g. as activator or antitumor agent, also induces
PI cytotoxicity of killer cells
FS Claim 2, Page 22, 20FP, English.
CC This sequence represents the interferon gamma (IFNgamma) inducer protein
CC of the liver tumor. This protein induces IFNgamma production in
CC immunocompetent cells. The protein is useful as an antiviral
CC antitumor, anti-septic, immunoregulatory and platelet-increasing agent.
CC It can be used for treatment or prevention AIDS, Hodgkin's lymphoma,
CC renal of brain cancer, glioblastoma, myeloid leukemia, rheumatism and
CC allergy. The protein can also be used to induce IFNgamma production in
CC cultured cells. The IFNgamma inducer strongly induces cytotoxicity of
CC killer T cells and when used with interleukin-2 (IL-2) and tumor
CC necrosis factor (TNF), may improve the effect (or induce side effects) of
CC adoptive immunotherapy in humans. The DNA encoding this sequence can
CC be used to produce the protein, which can then be purified (if assayed)
CC using monoclonal antibodies.
SQ Sequence 157 AA:

Query Match 100.0% Score 31, DB 1, Length 157;
best local similarity 100.0%, P03, No 2.5,
Matches 6: Conservative 0: Mismatches 0: Indels 0: Gaps 0

Q1 1 NDVLF 6
|||||
DB 16 NDVLF 21

RESULT 2
R92564
AC R92564 standard: Protein, 157 AA.
DE 29-SEP-1996 (first entry)
DE Human interferon gamma inducer protein.
KW Interferon-gamma inducer protein, IFN-gamma, antitumor, cytokine,
KW anti-tumor, antiseptic, immunoregulatory, platelet increasing agent,
KW theophylline, sodium acetate, renal cancer, brain cancer,
KW 910-1504, myeloid leukemia, rheumatism, allergy, cytokine, AIDS,
KW Interleukin, interleukin, IL-18, tumor necrosis factor (TNF),
KW adoptive immunotherapy, monoclonal antibody.
OS Homo sapiens.
FH key Location/Qualifiers

100.0% Score 31: DB 1: Length 157;
 Best Local Similarity 100.0%; Pred. No. 2.5;
 Matches 6: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

11 NOV-1994: JP-304203.
 23-FEB-1995: JP-058240.
 10-MAR-1995: JP-078357.
 18-SEP-1995: JP-262062.
 29-SEP-1995: JP-274988.
 (HAYB) HAYASHIBARA SEIICHIRO KAGAKU
 Fukuda S., Kohno K., Kunitaka T., Kurimoto M., Okamura H.
 Taniguchi M., Tanimoto T., Toriige K., Ushio S.
 N-PSDB: T32403.
 WPI: 96-252837/26.
 DR N-PSDB: T32403.
 Example A 3-2, Page 36 37, 48pp, English.
 A novel mouse protein (P99559) induces interferon-gamma (IFN-gamma)
 CC prodn. by immunocompetent cells. Its sequence was deduced from
 CC that of a cDNA clone (T32403) isolated from a mouse liver library.
 CC Recombinant IFN-gamma inducer protein can be produced in high yields
 CC using host cells, esp. Escherichia coli, transformed with a vector
 CC carrying the cDNA.
 CC Sequence 157 AA:

11 NOV-1994: JP-304203.
 23-FEB-1995: JP-058240.
 10-MAR-1995: JP-078357.
 18-SEP-1995: JP-262062.
 29-SEP-1995: JP-274988.
 (HAYB) HAYASHIBARA SEIICHIRO KAGAKU
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 N-PSDB: T32403.
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 DR N-PSDB: T32403.
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 CC prodn. by immunocompetent cells. Its sequence was deduced from
 CC that of a cDNA clone (T32403) isolated from a mouse liver library.
 CC Recombinant IFN-gamma inducer protein can be produced in high yields
 CC using host cells, esp. Escherichia coli, transformed with a vector
 CC carrying the cDNA.
 CC Sequence 157 AA:

NK cells, lymphokine-activating killer (LAK) cells, and cytotoxic
 T-cells). Recombinant IFN-gamma inducer protein can be produced in
 high yields using host cells, esp. Escherichia coli, transformed
 with a vector carrying the cDNA (T32403). It is useful
 as an antiviral, antitumor, antibacterial, immunoregulatory and
 blood platelet enhancing agent, and can be used in adoptive
 immunotherapy. It is also used to raise monoclonal antibodies.
 A full length sequence is given in R99560.
 Sequence 157 AA:

11 NOV-1994: JP-304203.
 23-FEB-1995: JP-058240.
 10-MAR-1995: JP-078357.
 18-SEP-1995: JP-262062.
 29-SEP-1995: JP-274988.
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 Fukuda S., Kohno K., Kunitaka T., Kurimoto M., Okamura H.
 Taniguchi M., Tanimoto T., Toriige K., Ushio S.
 N-PSDB: T32403.
 WPI: 96-252837/26.
 DR N-PSDB: T32403.
 Example A 3-2, Page 36 37, 48pp, English.
 A novel mouse protein (P99559) induces interferon-gamma (IFN-gamma)
 CC prodn. by immunocompetent cells. Its sequence was deduced from
 CC that of a cDNA clone (T32403) isolated from a mouse liver library.
 CC Recombinant IFN-gamma inducer protein can be produced in high yields
 CC using host cells, esp. Escherichia coli, transformed with a vector
 CC carrying the cDNA.
 CC Sequence 157 AA:

11 NOV-1994: JP-304203.
 23-FEB-1995: JP-058240.
 10-MAR-1995: JP-078357.
 18-SEP-1995: JP-262062.
 29-SEP-1995: JP-274988.
 (HAYB) HAYASHIBARA SEIICHIRO KAGAKU
 Fukuda S., Kohno K., Kunitaka T., Kurimoto M., Okamura H.
 Taniguchi M., Tanimoto T., Toriige K., Ushio S.
 N-PSDB: T32403.
 WPI: 96-252837/26.
 DR N-PSDB: T32403.
 Example A 3-2, Page 36 37, 48pp, English.
 A novel mouse protein (P99559) induces interferon-gamma (IFN-gamma)
 CC prodn. by immunocompetent cells. Its sequence was deduced from
 CC that of a cDNA clone (T32403) isolated from a mouse liver library.
 CC Recombinant IFN-gamma inducer protein can be produced in high yields
 CC using host cells, esp. Escherichia coli, transformed with a vector
 CC carrying the cDNA.
 CC Sequence 157 AA:

CC or treata IGIF-2 induction of proliferation, decreased induction of maturation
 CC of leukocytes or lymphocytes, especially in relation to the disease state
 CC associated with inflammation.
 SO Sequence 193 AA;

QY 1 NDQVLF 6 100.0% Score 31; DB 1; Length 193;
 Best Local Similarity 100.0%; Pred. No. 3.2;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps

SO 52 NDQVLF 57
 QY 1 NDQVLF 6
 SO Sequence 157 AA;

RESULT 10
 W15704
 W15704 standard; peptide: 157 AA.
 AC W15704;
 FT 26-JAN-1999 (first entry)
 FT Mouse interferon gamma inducer protein.
 KW Interferon-gamma, IFN-gamma, antiviral, antiproliferative therapy;
 KW immunoreactivity, antitumor agent, chemotherapy, neoplasia;
 KW thrombocytopaenia, immunocompetent cell; asthma; hayfever;
 KW rheumatism; interleukin; killer cell.
 OS Mus musculus.
 PH Key
 FT Misc-difference 70
 FT /label= Met, Thr
 FT EP 757178-AA.
 FT 09-APR-1997.
 PD 26-SEP-1996; 306997.
 PR 20-SEP-1996; JP-269105.
 PR 26-SEP-1995; JP-270725.
 PR 29-FEB-1996; JP-067434.
 PA (HAY) HAYASHIRAPA SEITOTSU KAGAKU.
 PI Akita K, Fujii M, Kurimoto M, Nakada Y, Tanimoto T;
 WP: 97-205381/19.
 DR N-PSDB; 160536.
 PR Human protein that induces interferon-gamma prodn. It
 PI immunocompetent cells - useful for adoptive immunotherapy of
 PI tumours and as antimicrobial agent etc.
 PS Disclosure: Page 23; 26pp; English.
 CC The present sequence represents a novel protein from mouse liver cells,
 CC which induces interferon gamma (IFN gamma) production in immunocompetent
 CC cells. This protein enhances cytotoxicity of killer cells and induces
 CC their formation. It is used as an antiproliferic agent for antitumor
 CC immunotherapy, an antiviral (including anti-AIDS) or antibacterial agent
 CC and in the treatment of allergic or immune system diseases, e.g. asthma,
 CC hayfever or rheumatism. When formulated with interleukin 3, it is also
 CC used to treat leukopenia and thrombocytopaenia associated with
 CC radiotherapy or chemotherapy of leukemia and other cancers. When used
 CC in antitumor immunotherapy, this novel protein synergistically improves
 CC the immunotherapeutic effect of interleukin-2 (IL-2), compared with use
 CC of IL-2 alone, either when administered to the patient (before
 CC administration of IL-2) or by addition to the medium in which cells
 CC (intended for return to the patient) are being grown.
 SO Sequence 157 AA;

QY 1 NDQVLF 6 100.0% Score 31; DB 1; Length 157;
 Best Local Similarity 100.0%; Pred. No. 2.5;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps

SO 16 NDQVLF 21
 QY 1 NDQVLF 6
 SO Sequence 157 AA;

RESULT 11
 W15697
 W15697 standard; peptide: 50 AA.
 AC W15697;
 FT 01-APR-1997 (first entry)
 FT Mouse interferon gamma inducer protein.
 KW Interferon-gamma, IFN-gamma, antiviral, antiproliferative therapy;
 KW immunoreactivity, antitumor agent, chemotherapy, neoplasia;
 KW thrombocytopaenia, immunocompetent cell; asthma; hayfever;
 KW rheumatism; interleukin; killer cell.
 OS Mus musculus.
 PH Key
 FT Misc-difference 70
 FT /label= Met, Thr
 FT EP 757178-AA.
 FT 09-APR-1997.
 PD 26-SEP-1996; 306997.
 PR 20-SEP-1996; JP-269105.
 PR 26-SEP-1995; JP-270725.
 PR 29-FEB-1996; JP-067434.
 PA (HAY) HAYASHIRAPA SEITOTSU KAGAKU.
 PI Akita K, Fujii M, Kurimoto M, Nakada Y, Tanimoto T;
 WP: 97-205381/19.
 DR N-PSDB; 160536.
 PR Human protein that induces interferon-gamma prodn. It
 PI immunocompetent cells - useful for adoptive immunotherapy of
 PI tumours and as antimicrobial agent etc.
 PS Disclosure: Page 23; 26pp; English.
 CC The present sequence represents a novel protein from mouse liver cells,
 CC which induces interferon gamma (IFN gamma) production in immunocompetent
 CC cells. This protein enhances cytotoxicity of killer cells and induces
 CC their formation. It is used as an antiproliferic agent for antitumor
 CC immunotherapy, an antiviral (including anti-AIDS) or antibacterial agent
 CC and in the treatment of allergic or immune system diseases, e.g. asthma,
 CC hayfever or rheumatism. When formulated with interleukin 3, it is also
 CC used to treat leukopenia and thrombocytopaenia associated with
 CC radiotherapy or chemotherapy of leukemia and other cancers. When used
 CC in antitumor immunotherapy, this novel protein synergistically improves
 CC the immunotherapeutic effect of interleukin-2 (IL-2), compared with use
 CC of IL-2 alone, either when administered to the patient (before
 CC administration of IL-2) or by addition to the medium in which cells
 CC (intended for return to the patient) are being grown.
 SO Sequence 157 AA;

2007 Mitch 000, 44 Spec: 28; DB 1; length 110;
6089 L. al. 000, 44 Prod. No. 6;
Mammals 1; Mammals 0; Indels 0; Gaps 0;

[illegible][illegible][illegible]

NAME	NO. 44	SCORE	28	DB	1	Length	110
John March							
Robert Lovell							
Samuel S. Hart							
Marjorie E. Thompson							
NOV 10							
NOV 11							
NOV 12							
NOV 13							
NOV 14							
NOV 15							
NOV 16							
NOV 17							
NOV 18							
NOV 19							
NOV 20							
NOV 21							
NOV 22							
NOV 23							
NOV 24							
NOV 25							
NOV 26							
NOV 27							
NOV 28							
NOV 29							
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NOV 36							
NOV 37							
NOV 38							
NOV 39							
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NOV 41							
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NOV 70							
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NOV 72							
NOV 73							
NOV 74							
NOV 75							
NOV 76							
NOV 77							
NOV 78							
NOV 79							
NOV 80							
NOV 81							

BRISTOL, R. A. and LINDO, P. W. 1976. Vaccinia virus (strain WR, 65-16) and its use as a vaccine against smallpox. *Journal of the Royal Society of Medicine*, **69**, 11-14.

Received 10 April 2006; accepted 12 July 2006
Published online 12 September 2006 in Wiley InterScience (www.interscience.wiley.com). DOI: 10.1002/jbm.b.30377

Query Match	90.3%	Score 28	DB 1	Length 136
Best Local Similarity	83.4%	Pred. No. 7.6		
Matches	Conservative 1	Mismatches	Indels 0	Deletions 0

Qy	1	ND0VLF	6
Db	101	NDEVLf	106

RESULT 6
C64438

phenylalanine-tRNA ligase (EC 6.1.1.20) beta chain - *Methanococcus jannaschii*
 N: Alternate names: phenylalanyl-tRNA synthetase, subunit beta
 C: Species: *Methanococcus jannaschii*
 C: Date: 13-Sep-1994 #sequence_revision 13-Sep-1994 #text_revision 21-Nov-1994
 #accession: C64438

R. Bult, G. J. White, O. Olson, G. J. Esho, T. Pitselakou, R. Saito, I. N. Pavlou, C. Welch, C. J. Overbeek, R. Kirksess, B. F. Wainlock, K. G. Morrish, J. M. Stokk, J. D. Sadow, P. W. Hanna, M. C. Cotton, M. D. Roberts, K. H. Harrell, M. A. Kalne, Science 273, 1058-1071, 1996

Authors: Borodovsky, M., Elcock, J. D.

A.Title: Complete genome sequence of the methanogenic archaeon, *Methanopyrus kandleri* AV19.
A.Reference number: A64100. Mftp:66377999
A.Accession: C6438
A.Status: preliminary; nucleic acid sequence not shown; translation not shown
A.Location: genome; complete
A.Distribution: available

A: nucleotide sequence type: DNA
 A: residues: 1-548 /BOL
 A: cross-references: 22:567553, GB:177117, NID:q1591744, PIR:q1591750, 158:MI1134; PI
 C: Geneticals:
 A: Map position: PEV1048809..1047162

Query Match 99.3% Score 29.734 E 1e-075 546
 Csuperfamily: Yeast cytosolic phenylalanine-tRNA ligase alpha chain
 K: keywords: aminocyl-tRNA synthetase; ligase; protein biosynthesis

Best Local Similarity	83.38	Pred. No. 37	Random 96%
Matches	5	Conservative	1
		Mismatches	6
		Inserts	0
		Gaps	0
1	NDGYLF	5	
1	1	1	1

390	NDEVLP	395
7	RESULT	
AA1029		
AA1029		

Interleukin beta-8 chain precursor - human
 Species: Homo sapiens (man)
 Date: 30-Jun-1992 #sequence=10 #translation=10
 Accession: A41029 #text=database 06 Sep-1992

1. Kroyer, M.; Napier, M.A.; McLean, J.W.
J. Biol. Chem. 266, 19650-19658, 1991.
 2. Title: Cloning and expression of a divergent integrin subunit beta-8.
 3. Reference number: A41029; MJD:92011767
 4. Accession: A41029

Molecule type: mRNA
 Accession: 1-760 -MOT
 Cross-references: GR-M73760; N10-9194520 PIP 3181-21
 Similarity: integrin beta chain
 Keywords: cell adhesion; extracellular matrix; distribution

Query Match: 76.8% Score: 33; DB: 2; Length: 769;
Best Local Similarity: 83.3%; Pred. No: 54;

Matches 5: Conservative 1: Mismatches 0: Indels 0: Gaps 0:
 QY 1 NDVLF 6
 |||||
 Db 425 NDEVLF 430

RESULT 8
 S29911

hypothetical protein 5 - vaccinia virus

C:Species: vaccinia virus

C>Date: 20-Feb-1997 #sequence_revision 20-Feb-1995 #text_change 08-Sep-1997

C:Accession: S29911

R:Amegadze, B.Y. submitted to the EMBL Data Library, January 1991

A:Reference number: S29907

A:Accession: S29911

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1110 <MB>

A:Cross-references: EMBL:X7318, NID:3404280, PID:3404284

C:Superfamily: vaccinia virus 14k cell fusion protein

Query Match 90.3% Score 28: DB 2: Length 110:
 Best Local Similarity 83.3% Pred. No. 6:
 Matches 5: Conservative 1: Mismatches 0: Indels 0: Gaps 0:

QY 1 NDVLF 6
 |||||
 Db 75 NDEVLF 80

RESULT 9
 S37292

fusion protein, 14k - Escherichia virus

C:Species: Escherichia virus

C>Date: 06-Jun-1997 #sequence_revision 26-May-1995 #text_change 08-Sep-1997

C:Accession: S37292

R:Kreyer, H., Osterrieder, X.Y.Z., Gorny, X.Y.Z. submitted to the EMBL Data Library, September 1993

A:Description: Identification of binding sites for neutralizing mabs.

A:Reference number: S37274

A:Accession: S37282

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1110 <MB>

A:Cross-references: EMBL:X7157, NID:3404280, PID:3404281

A:Note: The fusion is designated as monkeypox virus

C:Superfamily: vaccinia virus 14k cell fusion protein

Query Match 90.3% Score 28: DB 2: Length 110:
 Best Local Similarity 83.3% Pred. No. 6:
 Matches 5: Conservative 1: Mismatches 0: Indels 0: Gaps 0:

QY 1 NDVLF 6
 |||||
 Db 75 NDEVLF 80

RESULT 10
 S37281

fusion protein, 14k - monkeypox virus

C:Species: monkeypox virus

C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 08-Sep-1997

C:Accession: S37281

R:Kreyer, H., Osterrieder, X.Y.Z., Gorny, X.Y.Z. submitted to the EMBL Data Library, September 1993

A:Description: Identification of binding sites for neutralizing mabs.

A:Reference number: S37274

A:Accession: S37281

A:Status: preliminary

A:Molecule type: DNA
 A:Residues: 1110 <MB>
 A:Cross-references: EMBL:X7156, NID:3404278, PID:3404279
 C:Superfamily: vaccinia virus 14k cell fusion protein

Query Match 90.3% Score 28: DB 2: Length 110:
 Best Local Similarity 83.3% Pred. No. 6:
 Matches 5: Conservative 1: Mismatches 0: Indels 0: Gaps 0:

QY 1 NDVLF 6
 |||||
 Db 75 NDEVLF 80

RESULT 11
 S37275

fusion protein, 14k - cowpox virus

C:Species: cowpox virus

C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 08-Sep-1997

C:Accession: S37275

R:Kreyer, H., Osterrieder, X.Y.Z., Gorny, X.Y.Z. submitted to the EMBL Data Library, September 1993

A:Description: Identification of binding sites for neutralizing mabs.

A:Reference number: S37274

A:Accession: S37275

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1110 <MB>

A:Cross-references: EMBL:X7156, NID:3404280, PID:3404284

C:Superfamily: vaccinia virus 14k cell fusion protein

Query Match 90.3% Score 28: DB 2: Length 110:
 Best Local Similarity 83.3% Pred. No. 6:
 Matches 5: Conservative 1: Mismatches 0: Indels 0: Gaps 0:

QY 1 NDVLF 6
 |||||
 Db 75 NDEVLF 80

RESULT 12
 S37274

fusion protein, 14k - camelpox virus

C:Species: camelpox virus

C>Date: 06-Jun-1997 #sequence_revision 06-Jun-1995 #text_change 08-Sep-1997

C:Accession: S37274

R:Kreyer, H., Osterrieder, X.Y.Z., Gorny, X.Y.Z. submitted to the EMBL Data Library, September 1993

A:Description: Identification of binding sites for neutralizing mabs.

A:Reference number: S37274

A:Accession: S37274

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1117 <MB>

A:Cross-references: EMBL:X7156, NID:3404281, PID:3404282

C:Superfamily: vaccinia virus 14k cell fusion protein

Query Match 90.3% Score 28: DB 2: Length 117:
 Best Local Similarity 83.3% Pred. No. 6:
 Matches 5: Conservative 1: Mismatches 0: Indels 0: Gaps 0:

QY 1 NDVLF 6
 |||||
 Db 75 NDEVLF 80

RESULT 13

A:Accession: S37281
 A:Status: preliminary
 C:Species: Escherichia coli

NC ARCHAEA: EURYARCHAEOTA: METHANOBACTERIALES: METHANOBACILLARIACEAE

RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2.
RA GIBBEL C.O. BRADSHAW H. J.
RL SUBMITTED 1991-1990 TO EMBL/GENBANK/EBD3 DATA BANKS
RN 13.
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2.
RA WATERSTON R. J.
RL SUBMITTED (JUL-1996) TO EMBL/GENBANK/EBD3 DATA BANKS
RR EMBL: 354840, 3446791; -
SQ SEQUENCE 308 AA: 42376 MW: 44330.04A GPG72-

OC PHRYGAEOTA: METAFYCA: NEMATODA: SECEPHALANTHA: PHAEOTHIA: PHAEOTHIDA:
OC PHAEOTHIA: PHAEOTHIDA: PHAEOTHIDA: PELODERMINA: IACONOPHAGOTIS.
EN [1]
RD SOURCE FROM N.A.

QY	1	FEEMTD	6
	1	1	1
DB	26	FEEMTD	31

RESULT 13

```

053682
1D 053682
AC 053682
DT 01-NOV-1996 (REMBELFEL 01, CREATED)
DT 01-NOV-1996 (REMBELFEL 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1996 (REMBELFEL 08, LAST ANNOTATION UPDATE)
DE PROTECTIN BINDING PROTEIN B.
ENDB.
OS STAPHYLOCOCCUS AUREUS.
OC BACTERIA, GRAM-POSITIVE, BACILLUS/STAPHYLOCOCCUS GROUP: BACILLACEAE.
OC STAPHYLOCOCCUS.
PN 11)
RZ SEQUENCE FROM N.A.
RC STRAIN:922014.
RX MEDLINE: 9211475.
FA TANSON R. STANAS C. MULLIF H P. LINDEBERG M.
RT TWO DIFFERENT GENES ENCODE PROTECTIN BINDING PROTEINS IN
RT STAPHYLOCOCCUS AUREUS. THE COMPLETE NUCLEOTIDE SEQUENCE AND
RT CHARACTERIZATION OF THE SECOND GENE.
RT PIP. AbstrHEW 200141-1042(1993).
DE DBL: 9202014 DE
DE EMBL: X62014 DE
DE EMBL PROTEIN: C12759.1 DE
DE SEQUENCE: 340 AA; 10355 MW; 2584050 CPOSS.

```

[illegible]

RESULT	14			
077073				
ID	077073	PRELIMINARY	PR.	92 AA.
AC	077073			
DI	01-NOV-1996	(REMBREL, 01, CREATED)		
DI	01-NOV-1996	(REMBREL, 01, LAST SEQUENCE UPDATE)		
DT	01-NOV-1996	(REMBREL, 01, LAST ANNOTATION UPDATE)		
DE	ENVELOPE PROTEIN (FRAGMENT).			
CN	ENV.			
OS	HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (HIV-1).			
OC	RETROVIRUS; RETROVIRUS; RETROVIRIDAE; LENTIVIRUS.			
RN	(1)			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-PATIENT MOTHER 566, 24-MONTH SAMPLE;			
RA	SIMONON A. KAMPESSA G.A., VAN DE PEPPE P., KAPITA F., MSELATI P.,			
RA	KIRKEN C., GOODSMITH J.,			
FI	SUBMITTED (JUL-1996) TO EMBL/GENBANK/DBJ DATA BANKS.			
DR	EMBL: Z76036, E254051.			
KW	ENVELOPE PROTEIN.			
FT	NON-TER			
FT	NON-TER			
FT	NON-TER			
FO	SEQUENCE	92 AA.	1077073 MB.	AD8EB164 CRO322.

```

Query: Match 0: 0, Seed 0, E 11, Length 32,
      Best Local Similarity 32.34, Pval No. 12,
      Matches 5, Conservative 1, Mismatches 0, Gaps 0,
      QY 1, EEDMD 6,
      111111,
      5, FEDMD 10,
      26

```

RESULT	15	
Q76599		
ID	C74494	PRELIMINARY:
AC	Q76599	PRT:
DI	01-NOV-1996	92 AA.
DI	01-NOV-1996	(FRENCHBEL, 01, CREATED)
DI	01-NOV-1996	(FRENCHBEL, 01, LAST SEQUENCE UPDATED)

DI 01-INV-1466 (TREMURFEL 08 LASTI ANNAMALION UPDATE)
DE ENVELOPE PROTEIN (FRAGMENT).
CN ENV.
OS HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (HIV-1).
OS VIF/RSR1; RETROVIRUS; RETROVIRIDAE; LENTIVIRUS.
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN-PATIENT CHILD 566, 24-MONTH SAMPLE;
RA SIMONON A., KAMPEUGA G.A., VAN DE PERRE P., KARITA E., MESTRETTI F.,
KA KUIKEN C., GOODSMIT J., EMELDENBANK/ICRT DATA BANKS.
RF S98P01166 (001-1986) 10; EMELDENBANK/ICRT DATA BANKS.
DE EMBL; E02063; E25624; 1.
DR PRAM; P000516; GP120; 1.
KM ENVELOPE PROTEIN.
FT NON TER 1
FT NON TER 92 92
FT NON TER 1
SQ SEQUENCE 92 AA; 10522 MW; 551692200 CRC62;

Cover	Maintain	87-99	500-99	DR	111	Leads	99
Belt	Loose	60-89	Exo	No. 12			
Materials	Fabricated	60-89					
	Conservation						
OY	1 FEMTD	6					
Eb	5 FEMTD	10					

```
Searched complete. Time = 0.00 sec
Job time: 167 sec
```



GenScore version 4.5
Copyright (c) 1993 - 1998 CompuGen Ltd.

OM Protein - protein search, using sw model

Run on: June 22, 1999, 10:56:39 : Search time 51.72 seconds

(without alignments)
2.294 Million cell updates/sec

Title: US-09-030-061-3

Perfect score: 32

Sequence: 1 FRILKK 7

Scoring table: BLOSUM62

Search: 10000 seqs, 20000000 residues

Database: A_Geneseq_34

Prod. No. is the number of results predicted by chance to have a
Score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	33	100.0	157	1	R92506	Interferon gamma p
2	33	100.0	157	1	R92564	Human Interferon-g
3	33	100.0	157	1	R92558	Human mature inter
4	33	100.0	157	1	R92559	Mouse mature inter
5	33	100.0	157	1	R92560	Human Interferon-g
6	33	100.0	157	1	R92562	Mouse protein for
7	33	100.0	157	1	R92566	Human Interferon-g
8	33	100.0	157	1	R92567	Interferon gamma i
9	33	100.0	157	1	R92568	Interferon gamma i
10	33	100.0	157	1	R92569	Mouse Interferon-g
11	33	100.0	157	1	R92570	Interferon gamma i
12	33	100.0	157	1	R92571	Amino acid sequenc
13	33	100.0	157	1	R92572	Interferon gamma i
14	33	100.0	157	1	R92573	Interferon gamma i
15	33	100.0	157	1	R92574	Interferon gamma i
16	33	100.0	157	1	R92575	Interferon gamma i
17	33	100.0	157	1	R92576	Interferon gamma i
18	33	100.0	157	1	R92577	Interferon gamma i
19	33	100.0	157	1	R92578	Interferon gamma i
20	33	100.0	157	1	R92579	Interferon gamma i
21	33	100.0	157	1	R92580	Interferon gamma i
22	33	100.0	157	1	R92581	Interferon gamma i
23	33	100.0	157	1	R92582	Interferon gamma i
24	33	100.0	157	1	R92583	Interferon gamma i
25	33	100.0	157	1	R92584	Interferon gamma i
26	33	100.0	157	1	R92585	Interferon gamma i
27	33	100.0	157	1	R92586	Interferon gamma i
28	33	100.0	157	1	R92587	Interferon gamma i
29	33	100.0	157	1	R92588	Interferon gamma i
30	33	100.0	157	1	R92589	Interferon gamma i
31	33	100.0	157	1	R92590	Interferon gamma i
32	33	100.0	157	1	R92591	Interferon gamma i
33	33	100.0	157	1	R92592	Interferon gamma i
34	33	100.0	157	1	R92593	Interferon gamma i
35	33	100.0	157	1	R92594	Interferon gamma i
36	33	100.0	157	1	R92595	Interferon gamma i
37	33	100.0	157	1	R92596	Interferon gamma i
38	33	100.0	157	1	R92597	Interferon gamma i
39	33	100.0	157	1	R92598	Interferon gamma i
40	33	100.0	157	1	R92599	Interferon gamma i
41	33	100.0	157	1	R92600	Interferon gamma i
42	33	100.0	157	1	R92601	Interferon gamma i
43	33	100.0	157	1	R92602	Interferon gamma i
44	33	100.0	157	1	R92603	Interferon gamma i
45	33	100.0	157	1	R92604	Interferon gamma i

ALIGNMENTS

RESULT	1	44	33	100.0	157	1	W77093
1	R92506	45	33	100.0	157	1	W77098
2	R92506						Human Interleukin-
3	R92506						
4	R92506						
5	R92506						
6	R92506						
7	R92506						
8	R92506						
9	R92506						
10	R92506						
11	R92506						
12	R92506						
13	R92506						
14	R92506						
15	R92506						
16	R92506						
17	R92506						
18	R92506						
19	R92506						
20	R92506						
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35	R92506						
36	R92506						
37	R92506						
38	R92506						
39	R92506						
40	R92506						
41	R92506						
42	R92506						
43	R92506						
44	R92506						
45	R92506						

NK cells. Impacking activating killer (AK) cells and cytokines
 CC T cells. Embryonic IFN-gamma inducible protein can be produced in
 CC high yields using host cells, esp. Escherichia coli. Transformed
 CC with a vector carrying the encoding cDNA (722402). It is used
 CC as an antiviral, antitumor, antibacterial, immunomodulatory and
 CC blood platelet enhancing agent, and can be used in adoptive
 CC immunotherapy. It is also used to raise protective antibodies.
 CC A full-length sequence is given in R09650.
 SO Sequence 157 AA;

Query Match 100.0% Score 53; LR 1; Length 157
 Heat Local Similarity Low.0% Pred. No. 2, 3;
 Matches 2, Conservative 0, Mismatches 0, Indels 1, Gaps 0

Cy 1 FILLKK 7
 Db 134 FILLKK 140

RESULT 4
 R09559
 ID 50555 Standard: Protein; 157 AA.
 AC R09559;
 DT 29-SEP-1995 (first entry)
 DE Mouse murine interferon-gamma inducer protein.
 KW Interferon-gamma induced protein; IFN-gamma; antiviral; viral; ant
 KW antitumor; antibacterial; immunoregulator; adaptive induction; therapy
 KW therapy; cancer.

```

FT      misc_difference 70
FD      /label= Ile, Thr
FE      719931-AA.
FN
FP      22-MAY-1996.
FR      10-NOV-1995; JP-08055.
FS      15-NOV-1994; JP-704203.
FC      23-FEB-1995; JP-058240.
GT      10-MAR-1995; JP-078357.
PR      18-SEP-1995; JP-262052.
PS      29-SEP-1995; JP-274988.
PA      (HAYB.) HAYASHIBARA SEIICHIRO KAGAKU.
PI      FUKUDA S., KOSHO K., FUJIKURA T., KATSUMOTO M., OKAMURA H.
PL      Taniuchi M., Tanimoto I., Torihase K., Ushio S.
PP      WPI: 96-252897/26.
DR      N-PDBID: T32403.
DT      DNA encoding interferon gamma protein inducing polypeptide used
PT      to treat and prevent, e.g. viral disease, malignancies and immu-
PF      disorders.
PS      Example A-3-2: Page 36-37; 48pp; English.
CC      A novel mouse protein (R39559) induces interferon gamma (IFN-gamma)
CG      production by immunocompetent cells. Its sequence was deduced from
CC      that of a cDNA clone (T32403) isolated from a mouse liver library.
CC      Recombinant IFN-gamma inducer protein can be produced in high yields
CC      using host cells, esp. Escherichia coli, transformed with a vector
CC      carrying the cDNA.
SO      Sequence 157 AA.

Query Match          100.0%   Score 33; DB 1; Length 157;
Best Local Similarity 100.0%; Pred No. 2.3;
Matrix               Conservation 0; Mismatches 0; Indels 0; Gaps 0

27      1 FKLLKK 7
        | | | | | | |
DB       132 FKLLKK 138

RESULT      5
R99560
CDS         R99560:1..193 aa.
AA          R99560: 29-SEP-1996 (first entry)

```

DE Human interferon-gamma inducer protein.
 KW Interferon gamma inducing protein, IFN-gamma; antiviral; virocid;
 KW anti-tumour; anti-bacterial; immunoregulator; adoptive immunotherapy;
 KW +horipin; cancer.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT peptide 1..36
 FT /label= leader_peptide
 FT protein 37..193
 FT /label= Mat_protein
 FT misc_difference 109
 FT /label= Ile, Thr
 FT EP-712931.A2.
 PN 22 MAY-1995.
 PD 10-NOV-1995: 308055.
 PE 15-NOV-1994: JP-304203.
 PR 23-FEB-1995: JP-058240.
 PR 10-MAR-1995: JP-078357.
 PR 18-SEP-1995: JP-249062.
 PR 29-SEP-1995: JP-274988.
 PA (HAYR.) HAYASHIBARA SEIJIYOSU KAGAKU
 PI FUKUKI S. KOTOKI K. KUNITA T. KUNITA M. OKAMURA H.
 BI Tadavacho M. Tadavacho T. Tadavacho K. USHIO S.
 DR N-PSDB: T82404.
 FT DNA encoding for interferon-gamma protein-inducing polypeptide - useful
 PT to treat and prevent, e.g. viral disease, malignancies and immune
 PT disorders.
 PS Claim 6, Page 43-42, 48pp. English.
 CC The mature portion of a novel human protein (P99550) induces
 CC Interferon-gamma (IFN-gamma) prodn. by immunocompetent cells. It
 CC is the product of a cDNA clone (T32404) cp'd from a human liver
 CC library. The protein enhances the cytotoxicity of killer cells
 CC and/or induces the formation of killer cells (e.g. NK cells,
 CC lymphocyte-activating killer (LAK) cells, and cytotoxic T-cells)
 CC The mature protein (see also P99558) is useful as an antiviral,
 CC antitumor, antibacterial, immunoregulatory and blood platelet-
 CC enhancing agent and can be used in adoptive immunotherapy. It is
 CC also used to raise monoclonal antibodies.
 SO Sequence 133 AA.

Query Match 100.0% Score 33; DB 1; Length 193;
 Best Local Similarity 100.0% Prod. No. 2.9;
 Mismatches 0 Indels 0 Gaps 0

DE 1 FKILKK 7
 DB 170 FKILKK 175

RESULT 6
 W21252
 ID W24259 standard; Protein: 157 AA.
 AC W24252;
 DT 15-OCT-1997 (first entry)
 DE Marine protein for induction of interferon-gamma.
 DE Interferon gamma immunocompetent cell, malignant tumour;
 KW viral disease; bacterial infection; immune disease.
 OS Mus musculus.
 FH Key Location/Qualifiers
 FT misc_difference 70
 FT /note= "Encoded by AY1"
 FT J09157180-A.
 PN 17-JUN-1997.
 PD 24-JAN-1995: 028722.
 PE 04-OCT-1995: JP-279906.
 PR 10-MAR-1995: JP-078357.
 PR 29-SEP-1995: JP-274988.
 PA (HAYR.) HAYASHIBARA SEIJIYOSU KAGAKU
 PI WPI: 97-169361/34.
 DR N-PSDB: T82410.
 PT A drug containing a polypeptide which induces interferon-gamma -

PT useful for treating e.g. malignant tumours, viral, bacterial or
 PT immune diseases.
 PS Discovered, Page 10-11, 12pp. Japanese.
 CC This sequence represents a protein which induces interferon-gamma
 CC production in immunocompetent cells. This protein may be used as
 CC the major component in a drug for the prevention and treatment of
 CC e.g. malignant tumours, viral diseases, bacterial infections and
 CC immune diseases.
 SO Sequence 157 AA.

Query Match 100.0% Score 33; DB 1; Length 157;
 Best Local Similarity 100.0% Prod. No. 2.3;
 Mismatches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0

DE 1 FKILKK 7
 DB 132 FKILKK 138

RESULT 7
 W21258
 ID W24259 standard; Protein: 157 AA.
 AC W24258;
 DT 15-OCT-1997 (first entry)
 DE Human protein for induction of interferon-gamma.
 DE Interferon-gamma, immunocompetent cell; malignant tumour;
 KW viral disease; bacterial infection; immune disease.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT misc_difference 73
 FT /note= "Encoded by AY1"
 FT J09157180-A.
 PN 17-JUN-1997.
 PD 24-JAN-1995: 028722.
 PE 04-OCT-1995: JP-279906.
 PR 10-MAR-1995: JP-078357.
 PR 29-SEP-1995: JP-274988.
 PA (HAYR.) HAYASHIBARA SEIJIYOSU KAGAKU
 PI WPI: 97-169361/34.
 DR N-PSDB: T80209.
 PT A drug containing a polypeptide which induces interferon-gamma -
 PT useful for treating e.g. malignant tumours, viral, bacterial or
 PT immune diseases.
 PS Claim 1, Page 9, 12pp. Japanese.
 CC This sequence represents a protein which induces interferon-gamma
 CC production in immunocompetent cells. This protein may be used as
 CC the major component in a drug for the prevention and treatment of
 CC e.g. malignant tumours, viral diseases, bacterial infections and
 CC immune diseases.
 SO Sequence 157 AA.

Query Match 100.0% Score 33; DB 1; Length 157;
 Best Local Similarity 100.0% Prod. No. 2.3;
 Mismatches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0

DE 1 FKILKK 7
 DB 134 FKILKK 140

RESULT 8
 W31757
 ID W31757 standard; Protein: 143 AA.
 AC W31757;
 DT 15-JAN-1998 (first entry)
 DE Interferon gamma inducing factor 2 (IGIF-2) R1401 variant.
 DE Interferon gamma inducing factor 2, IGIF-2, hecocyte, lymphocyte; human;
 KW inflammation; interferon; interferon-inducer; microorganism; viral disease;
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT misc_difference 140

```

CC of liver tissue induction of epithelioid differentiation of macrophages
CC of dendritic cells, lymphocytes, especially in relation to fibroblasts
CC associated with inflammation.
SO Sequence 193 AA;

Query Match          100.0% Score 33 DB 1 Length 176
Best Local Similarity 100.0% Pred No. 28
Matches 7 Conservative 0 Mismatches 0 Indels 0 Gaps 0
CY 1 FKLLKK 7
      |||||
DB 170 FKLLKK 176

RESULT 10
W15704 W15704 standard, peptide: 157 AA.
W15704:
AC 26-JAN-1999 (first entry)
CT Mouse interferon-gamma inducer protein.
FE Interferon-gamma, IFN-gamma, antiviral; antiproliferative; radioprotective;
KW immunomodulatory; anti-tumor agent; chemotherapeutic leukopenia;
KM L-leucine-tyrosine; immunoregulatory cells (natural killer); hepatoma;
KM thymus; interleukin; killer cell).
OS Mus musculus.
FT Loc: 100/241/11/13
FT Misc-difference 70 /label= Mol, Thr
FT EP 767178-AA.
FN 09-APR-1997.
FD 26-SEP-1996: 306997.
PR 20-SEP-1996: JP-269105.
FR 26-SEP-1995: JP-267325.
RR 25-FEB-1995: JP-067434.
PA (HAYR.) HAYASHIRARA SEIICHIRO KAGAKU.
PI Akita K., Fujii M., Kurimoto M., Nakada Y., Tamoto T.
DR WP: 97.205381/19.
DR N-PSSD: T60536.
PT Human protein that induces interferon-gamma prom. in
PT Immunocompetent cells - useful for adoptive immunotherapy of
PT tumors and as antimicrobial agent etc.
PS Disclosure: Page 23, 25pp, English.
CC The present sequence represents a novel protein from mouse liver cells,
CC which induces interferon-gamma (IFN gamma) production in immunocompetent
CC cells. This protein enhances cytotoxicity of killer cells and induces
CC their formation. It is used as an antitumor agent for antitumor
CC immunotherapy, an antiviral (including anti-AIDS) or antibacterial agent
CC and in the treatment of atopic or immune system disease, e.g. asthma,
CC hay fever or rheumatism. When formulated with interleukin-3, it is also
CC used to treat leucopenia and thrombocytopenia associated with
CC radiotherapy or chemotherapy of leukemia and other cancers. When used
CC in antitumor immunotherapy, this novel protein significantly improves
CC the immunotherapeutic effect of interleukin-2 (IL-2) compared with use
CC of IL-2 alone, either when administered to the patient (before
CC administration of IL-2) or by addition to the medium in which cells
CC are cultured.
SO Sequence 157 AA;

Query Match          100.0% Score 33 DB 1 Length 157
Best Local Similarity 100.0% Pred No. 43
Matches 7 Conservative 0 Mismatches 0 Indels 0 Gaps 0
CY 1 FKLLKK 7
      |||||
DB 132 FKLLKK 138

RESULT 11
W15701 W15701 standard, protein: 157 AA.
W15701:
AC 26-JAN-1999 (first entry)
CT Mouse interferon-gamma inducer protein.
FE Interferon-gamma, IFN-gamma, antiviral; antiproliferative; radioprotective;
KW immunomodulatory; anti-tumor agent; chemotherapeutic leukopenia;
KM L-leucine-tyrosine; immunoregulatory cells (natural killer); hepatoma;
KM thymus; interleukin; killer cell).
OS Mus musculus.
FT Loc: 100/241/11/13
FT Misc-difference 70 /label= Mol, Thr
FT EP 767178-AA.
FN 09-APR-1997.
FD 26-SEP-1996: 306997.
PR 20-SEP-1996: JP-269105.
FR 26-SEP-1995: JP-267325.
RR 25-FEB-1995: JP-067434.
PA (HAYR.) HAYASHIRARA SEIICHIRO KAGAKU.
PI Akita K., Fujii M., Kurimoto M., Nakada Y., Tamoto T.
DR WP: 97.205381/19.
DR N-PSSD: T60536.
PT Human protein that induces interferon-gamma prom. in
PT Immunocompetent cells - useful for adoptive immunotherapy of
PT tumors and as antimicrobial agent etc.
PS Disclosure: Page 23, 25pp, English.
CC The present sequence represents a novel protein from mouse liver cells,
CC which induces interferon-gamma (IFN gamma) production in immunocompetent
CC cells. This protein enhances cytotoxicity of killer cells and induces
CC their formation. It is used as an antitumor agent for antitumor
CC immunotherapy, an antiviral (including anti-AIDS) or antibacterial agent
CC and in the treatment of atopic or immune system disease, e.g. asthma,
CC hay fever or rheumatism. When formulated with interleukin-3, it is also
CC used to treat leucopenia and thrombocytopenia associated with
CC radiotherapy or chemotherapy of leukemia and other cancers. When used
CC in antitumor immunotherapy, this novel protein significantly improves
CC the immunotherapeutic effect of interleukin-2 (IL-2) compared with use
CC of IL-2 alone, either when administered to the patient (before
CC administration of IL-2) or by addition to the medium in which cells
CC are cultured.
SO Sequence 157 AA;

```

DT 26-JAN-1993 (first entry)
DE Interferon gamma, human protein.
KW Interferon gamma, IFN-gamma, acti(vi)l, anti(viru)l, radiotherapy;
KW Immunoregulatory, antitumor agent; Chemotherapy; Leukemia;
KW Thymus; T cells; Immunogenicity; Cell killing; cytotoxic;
KW Rheumatism; Interleukin; killer cell
OS Homo sapiens.
FT Misc
FT Misc
FT Location/Qualifiers
FT Misc-difference 73
EN Ep-76/178-A;
EN 09-Apr-1997. /label= 1le, Thr
PD 26-SEP-1996; 306997.
PF 20-SEP-1996; TP-264105
PR 26-SEP-1997; TP-26675
PR 24-FEB-1996; TP-067434
PA (HAYR) HAYASHIRAPA SIENTSU KAGAKU
PI Akiyama, T.; Kikuchi, M.; Nakada, Y.; Tachibana, T.
PI WPI: 97-00684713
PT Human protein, the 19 kDa interferon-gamma protein in
PT immunocompetent cells, useful for adoptive immuno therapy of
PT tumors and as antitumoral agent etc.
PS Claim 8: Page 20; Cpp, English.
CC The present invention concerns a novel protein from human cells, which
CC induces interferon-gamma (IFN gamma) production in immunocompetent cells
CC and has antitumor effectiveness of killer cells and induces their
CC killing. It is used as an antitumor agent for antitumor
CC immunotherapy, as an adjuvant (including anti-IFN γ) of antitumor agent,
CC and in the treatment of allergic immune system diseases, e.g. asthma,
CC hay fever or rheumatism. When formulated with interleukin-3, it is also
CC used to treat leopopenia and thrombocytopaenia associated with
CC radiotherapy or chemotherapy of leukemia and other cancers. When used in
CC antitumor immunotherapy, this novel protein significantly improves the
CC immunotherapeutic effect of interleukin-3 (IL-3) compared with use of
CC IL-3 alone, either when administered to the patient (before
CC administration of IL-3) or by addition to the medium in which cells
CC (intended for return to the patient) are being grown.
SQ Sequence 157 AA;

FT	Region	/note="beta-2 region"
FT	Region	137..143
FT	Region	/note="beta-8 region"
FT	Region	147..153
FT	Region	/note="beta-3 region"
FT	Region	160..164
FT	Region	/note="beta-10 region"
FT	Region	170..175
FT	Region	/note="beta-11 region"
FT	Region	187..191
FT	Region	/note="beta-12 region"
FT	Region	
PD	27-NOV-1997	
PP	16-MAY-1997	007292.
PR	16-MAY-1997	US-0512593.
PA	(SCHEP) SCHEPING CORP.	
PI	Rajan TF, Hardiman GT, Kastelein PA, Sana TR, Timans JC;	
CR	WFO: 98 052327-02.	
NR	N-PSDR: W05368.	
RT	Antagonists of human interleukin-1 gamma used for the treatment of human immunological disorders caused by human IL-1 gamma	
PS	Disclosures: Pages 24-55; 63pp. English.	
CC	The present sequence represents human interleukin-1 gamma (IL-1 gamma). The protein is the human equivalent of a mouse cytokine, IL-1 gamma, which induces certain T cells to produce interferon gamma. Human IL-1 gamma and mouse IL1F show 70% identity at the nucleotide level and approximately 65% identity at the amino acid level. Antagonists of IL-1 gamma, e.g. antibodies, can be used in a method for treating a condition caused by human IL-1 gamma. The antibodies can also be used in diagnostic assays. The IL-1 gamma protein can be covalently conjugated to polymers, the type of a carrier polymer, and the fusion protein used in a pharmaceutical composition for supplying the biological activity of IL-1 gamma. Conditions that can be treated using the human IL-1 gamma receptor include immunological disorders, allergies, and infectious diseases. The IL-1 gamma can also be used to detect the presence of the protein or its receptor.	
SC	Sequence 192 AA;	

100.00: Score 33; DB 1; Length 193;
 Host Local Similarity 100.00; Pred. No. 2.8;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

100.00: Score 33; DB 1; Length 193;
 Host Local Similarity 100.00; Pred. No. 2.8;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

100.00: Score 33; DB 1; Length 193;
 Host Local Similarity 100.00; Pred. No. 2.8;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

100.00: Score 33; DB 1; Length 193;
 Host Local Similarity 100.00; Pred. No. 2.8;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

100.00: Score 33; DB 1; Length 193;
 Host Local Similarity 100.00; Pred. No. 2.8;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

100.00: Score 33; DB 1; Length 193;
 Host Local Similarity 100.00; Pred. No. 2.8;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

100.00: Score 33; DB 1; Length 193;
 Host Local Similarity 100.00; Pred. No. 2.8;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

W52172
 ID W52172 Standard: peptide: 193 AA.
 AC W52172;
 DT 10-JUN-1998 (first entry)
 DE Interferon-gamma inducing polypeptide precursor sequence.
 KW Interferon-gamma, IFN-gamma, precursor, enzyme, cleavage.
 OS Homo sapiens.
 FX Key: location/qualifiers
 FI Misc_difference 109
 FT EP-819757-A2.
 FN 41-JAN-1998;
 PD 18-JUL-1997; 305377.
 PE 30-MAY-1997; JP-156062.
 PR 19-JUL-1996; JP-207691.
 PA (HAYB.) HAYASHIBARA SEIBUTSU KAGAKU.
 PI Kurimoto M, Tanimoto T;
 DR WP1: 98-073838/08.
 DR N-PSDB: V17200.
 PT Polypeptide-processing enzyme for preparing mature form of
 PS Interferon-inducing polypeptide
 PS Claim 3; Page 15; 18pp; English.
 CC This sequence represents the precursor of an interferon-gamma (IFN-gamma)
 CC inducing polypeptide. The polypeptide induces IFN-gamma production in
 CC immunocompetent cells. The polypeptide is not named but is described in
 CC JP 27198/96 and 1998/96). An enzyme can convert this precursor form
 CC into its active form by cleaving a linkage between Asp at amino acid
 CC position 36 and Trp at amino acid position 37 of this terminal fragment.
 CC The enzyme can be obtained from a human hematopoietic cell and can be
 CC inhibited by isobutylamide and acetyl-L-tyrosyl-L-valyl-L-alanyl-L-aspart
 CC 1-al. The enzyme can be used for cleaving a recombinant IFN-gamma
 CC pro polypeptide to form a mature polypeptide.
 SC Sequence 193 AA;

Query Match 100.00: Score 33; DB 1; Length 193;
 Host Local Similarity 100.00; Pred. No. 2.8;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Search completed: June 22, 1999, 10:58:39
 Job time: 78 sec

RESULT 14

S74767

Hypothetical protein slr1066 - *Synechocystis* sp. (strain PCC 6803)C:Species: *Synechocystis* sp.

A:Variety: PCC 6803

C:Date: 25-Apr-1997 #sequence_revision: 25-Apr-1997 #text_change: 21-Aug-1998

C:Accession: S74767

R:Kobayashi, T., Saito, S., Kohata, H., Tanaka, A., Asanuma, E., Nakamura, Y., Miyajima, N.,

O. Kato, Chikara, S., Harada, S., Inaba, C., Wada, T., Watanabe, A., Yamada, M., Yasuda

DNA Res. 3, 109-116, 1996

A:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*

s.

A:Reference: PubMed: 871922, PMID:87061201

A:Accession: S74767

A>Status: Preliminary

A:Molecule type: DNA

A:Residues: 1401 (KARY)

A:Cross-reference: EMBL:U99001, GI:AB001339, NID:0161897, FID:0107051, FID:01651992

A:Note: the nucleotide sequence was submitted to the EMBL data library, June 1996

Query Match

84.8% Score 28; DB 2; Length 401;

Best local similarity 71.4%; Pred. No. 35;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERLIKK 7

111111

DB 139 ERLIKK 145

RESULT 15

S57149

Probable tentative histidine lyase, yeast (*Saccharomyces cerevisiae*)

N:Alternate names: hypothetical protein J7050

C:Species: *Saccharomyces cerevisiae*

C:Date: 23-Aug-1995 #sequence_revision: 06-Sep-1995 #text_change: 14-Nov-1997

C:Accession: S57149

R:Poser, M., Koeberle, P., Euliano, R.D.

submitted to the Protein Sequence Database, September 1995

A:Reference number: S56848

A:Accession: S57149

A:Molecule type: DNA

A:Residues: 1441 (KARY)

A:Cross-reference: EMBL:U99001, NID:0161897, FID:0107051, FID:01651992

C:Genetics:

A:Map position: 108

C:Keywords: transmembrane protein

Query Match

84.8% Score 28; DB 2; Length 811;

Best local similarity 71.4%; Pred. No. 71;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERLIKK 7

111111

DB 255 ERLIKK 261

Search completed: June 22, 1999, 10:58:47
Job time: 146 sec



[illegible]

50	SEQUENCE	194 AA	2213 MW	P9290270 C10032
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Query Match 87.9% Score 29 DB 10 Length 194
 Best Local Similarity 71.4% Prod. No. 36
 Matches 5 Conservative 2 Mismatches 0 Indels 0 Gaps 0

1 EFLIKK 7
 DB 169 PFLIKK 175

RESULT 6
 ID 055348 PRELIMINARY: PRT 551 AA
 AC 055348
 DT 01-JUN-1996 (TEMPREL: 05, CREATED)
 DT 01-JUN-1996 (TEMPREL: 05, LAST SEQUENCE UPDATE)
 DT 01-JUN-1996 (TEMPREL: 06, LAST ANNOTATION UPDATE)
 DE GLYCOPROTEIN G1 AND G2 PRECURSOR (FRAGMENT).
 OS MACIEL VIRUS.
 OC VIRUSSES: SSRNA NEGATIVE-STRAND VIRUSES: RUBNAVIRIDAE: HANTAVIRUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-B013796;
 RA LEVITS S., MORZUNOV S.P., POWE J.E., ENRIA D., PINT N., CALDERON G.,
 RA SABATINI M., ST JEOR S.C.;
 RL J. INFECT. DIS. 0:0-0(1998).
 DR EMBL: AF029227; 02653923; ..
 FT NON-TER 1
 FT NON-TER 551
 SQ SEQUENCE 551 AA: 11478 MW: 6419415.09142.

Query Match 87.9% Score 29 DB 11 Length 551
 Best Local Similarity 85.7% Prod. No. 96
 Matches 5 Conservative 1 Mismatches 0 Indels 0 Gaps 0

1 EFLIKK 7
 DB 60 PFLIKK 66

RESULT 7
 ID 055346 PRELIMINARY: PRT 1138 AA.
 AC 055346
 DT 01-JUN-1996 (TEMPREL: 05, CREATED)
 DT 01-JUN-1996 (TEMPREL: 06, LAST SEQUENCE UPDATE)
 DT 01-JUN-1996 (TEMPREL: 06, LAST ANNOTATION UPDATE)
 DE GLYCOPROTEIN G1 AND G2 PRECURSOR.
 OS ORAN VIRUS.
 OC VIRUSSES: SSRNA NEGATIVE-STRAND VIRUSES: RUBNAVIRIDAE: HANTAVIRUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-012255;
 RA LEVITS S., MORZUNOV S.P., POWE J.E., ENRIA D., PINT N., CALDERON G.,
 RA SABATINI M., ST JEOR S.C.;
 RL J. INFECT. DIS. 0:0-0(1998).
 DR EMBL: AF029227; 02653915; ..
 SQ SEQUENCE 1138 AA: 12748 MW: 6765367.09032.

Query Match 87.9% Score 29 DB 11 Length 1138;
 Best Local Similarity 85.7% Prod. No. 10002;
 Matches 5 Conservative 1 Mismatches 0 Indels 0 Gaps 0

1 EFLIKK 7
 DB 528 PFLIKK 534

RESULT 8
 ID 055349 PRELIMINARY: PRT 551 AA

AC 055349;
 DT 01-JUN-1996 (TEMPREL: 06, CREATED)
 DT 01-JUN-1996 (TEMPREL: 06, LAST SEQUENCE UPDATE)
 DT 01-JUN-1996 (TEMPREL: 05, LAST ANNOTATION UPDATE)
 DE GLYCOPROTEIN G1 AND G2 PRECURSOR (FRAGMENT).
 OS PERGAMINO VIRUS.
 OC VIRUSSES: SSRNA NEGATIVE-STRAND VIRUSES: RUBNAVIRIDAE: HANTAVIRUS.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-AA14403;
 RA LEVITS S., MORZUNOV S.P., POWE J.E., ENRIA D., PINT N., CALDERON G.,
 RA SABATINI M., ST JEOR S.C.;
 RL J. INFECT. DIS. 0:0-0(1998).
 DR EMBL: AF029228; 02653923; ..
 FT NON-TER 1
 FT NON-TER 551
 SQ SEQUENCE 551 AA: 61602 MW: 11090900.09032.

Query Match 87.9% Score 29 DB 11 Length 551;
 Best Local Similarity 85.7% Prod. No. 96;
 Matches 5 Conservative 1 Mismatches 0 Indels 0 Gaps 0

1 EFLIKK 7
 DB 60 PFLIKK 66

RESULT 9
 ID 006790 PRELIMINARY: PRT 258 AA.
 AC 006790
 DT 01-NOV-1996 (TEMPREL: 01, CREATED)
 DT 01-NOV-1996 (TEMPREL: 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1996 (TEMPREL: 06, LAST ANNOTATION UPDATE)
 DE GREEK PESTAL: PIRELLINE-3-CARBOXYLATE REDUCTASE (FRAGMENT).
 OS SACCAROMYCES CEREVISIAE (BAKERY'S YEAST).
 OC EUKARYOTA: FUNGI: ASCOMYCOTA: HEMIASCOMETES: SACCAROMYCETALES;
 OC SACCAROMYCETACEAE: SACCAROMYCES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SK02N;
 RA MEDLINER: 92374987;
 RA NEUVILLE P., ARIDE M.;
 RI "ore2", a mutation affecting proline biosynthesis in the yeast
 PI Sacccharomyces cerevisiae, locus to a odd phenotype.
 FT WOL. GEN. SECT. 241997.00011992).
 DR EMBL: X57248; 0434959; ..
 FT NON-TER 1
 SQ SEQUENCE 258 AA: 6998 MW: 5349546.09032.

Query Match 84.9% Score 29 DB 11 Length 258;
 Best Local Similarity 71.4% Prod. No. 77;
 Matches 5 Conservative 2 Mismatches 0 Indels 0 Gaps 0

1 EFLIKK 7
 DB 125 PFLIKK 131

RESULT 10
 ID 026049 PRELIMINARY: PRT 470 AA.
 AC 026049
 DT 01-NOV-1996 (TEMPREL: 01, CREATED)
 DT 01-NOV-1996 (TEMPREL: 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1996 (TEMPREL: 01, LAST ANNOTATION UPDATE)
 DE CELL SURFACE PROTEIN.
 OS PARACENTROTUS LIVIDUS (COMMON SEA URCHIN).
 OC EUKARYOTA: METAZOA: ECHINODERMATA: ECHINIDIA: ECHINACEA: EUDERMIDACEA;
 OC ECHINIDIA: ECHINIDIA: ECHINIDIA: PAPAENIDOTUS.

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DT 01-NOV-1996 (TREMELPEL 01 CREATED)
DT 01-NOV-1998 (TREMELPEL 08 LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMELPEL 08 LAST ANNOTATION UPDATE)
LN 500-4: 1:PROTEIN.
CN 500-4: 1:PROTEIN.
OS CAENORHABDITIS ELEGANS.
OC ELEGANTIA: NEMATODA: SPECERINTEA: RHABDITIA: RHABDITIA:
OC RHABDITIA: RHABDITIOIDEA: RHABDITIAE: PELODERINIA: CAENORHABDITIS
RN 11)
RF SOURCE: FROM N.A.
KL COTTAGE A.;
RN 12)
RP SOURCE: FROM N.A.
RX MEDLINE: 94150718.
HA WILSON R., AINSWORTH P., ANDERSON K., BAYNES C., BEERS M., BONFIELD
HA BOUTON J., CONNELL M., CORSEY T., DOOPER J., WILSON A., CRAXTON M.,
HA DEAR S., PITT J., PIRPIN P., FAVELL A., FITTON J., CAWNER A., GREEN P.,
HA HARRIS T., HILLIER L., JER M., JOHNSON L., JONES M., KRISHNA
HA KIRSTEN J., LAISTER N., LATREILLE P., LIGHTNING J., LLOYD G.,
HA MCGURRAY A., MORTIMORE B., O'CALLAGHAN M., PABINS J., PERCY
HA PIRKEN I., POOPRA A., SAUNDERS D., SHOWNKEN E., SHULTON N., SMITH A.,
HA SONNENMEYER E., STADEN P., STURTON J., THIERY-MERG S., THOMAS K.,
HA VAUDIN M., VAYRAN K., WATERSTON R., WATSON A., WEINSTEIN L.,
HA WILKINSON-SPOAT J., WOLFFMAN P.;
RN 2.2 Mb of contig300008 nucleotide sequence from chromosome 111 of C.
RT elegans.
RL NAUKA 36832-48(1994);
DR EMBL: Z68563; E1322451;
SO SEQUENCE 2010 AA; 43525 MW; 6774-B9C CRC64;

Query Match 84.8% Score 28; DB 3; Length 2810
Best Local Similarity 100.00; Freq. No. 76602;
Matches 5; Conservation 0; Mismatches 0; Gaps 0;
GY 1 FKILK 6
ID 11111
FB 1109 FKILK 1114

RESULT 13
ID 007446 PRELIMINARY: 197; 228 AA.
AC 007446:
DI 01-NOV-1996 (TREMELPEL 01 CREATED)
DT 01-NOV-1996 (TREMELPEL 01 LAST SEQUENCE UPDATE)
DI 01-NOV-1996 (TREMELPEL 08 LAST ANNOTATION UPDATE)
DE PEROXILASE 1 PELODIPSOR (EC 1.11.1.7);
CN TPX1.
OS LUTERASTION ESCULENTUM (TOMATO).
OC EGGAROVIA: VITICULANAE: CHACAPITIA/EGGAROVITIA: SPECERINTEA: EGGAROVITIA:
OC TRACHOPHYTES: EUPHYLLIPHYTES: SPERMATOPHYTES: MANCINIOPHYTES:
OC EUCOTYLEDONALES: ASTERIDAE: SOLANACEAE: SOLANALES: SOLANALES: SOLANACEAE: SOLANACEAE:
RN 11)
RF SEQUENCE: FROM N.A.
RX MEDLINE: 94302155.
HA BOELLA M. A., UTESAWA M. A., HASHIYAMA P. M., VALPUESTA V. J.;
RN "Nucleotide sequences of two peroxidase genes from tomato
RT (Lycopersicon esculentum)."
KL PLANT PHYSIOL. 103:653-664(1993).
OC 1- FUNCTION: REMOVAL OF H2O2(42); OXIDATION OF TOXIC METABOLITES;
OC BIOSYNTHESIS AND DEGRADATION OF LIGNIN; DEFENCE RESPONSE TOWARD
OC WOUNDING AND METABOLISM OF AUXIN; THESE FUNCTIONS MIGHT BE
OC DEPENDENT ON EACH ISOZYME/ISOPROTEIN IN EACH PLANT TISSUE.
OC 1 CATALYTIC ACTIVITY DONOR: H2O2(42) CATALYZED FROM F. 2 H2O(42)
OC 1 COFACTOR: THIS PROTEIN BINDS HEME.
DR EMBL: L13634; G678547;
DR PFAM: PF00141; peroxidase; 1;
CN 1:PEROXILASE1; LYCOPERSICON: PEROXILASES: HEMO: MYOGLUBIN: MYOGL:
KW SIGNAL. 1 22 POTENTIAL.

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SEQUENCE FROM N.A

Job time: 168 sec



[illegible]

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DE      83 MYKDS 87
      11111
RESULT  11
ID      W00399 standard: Protein; 197 AA.
AC      W00399;
DT      01-FEB-1997 (first entry)
DI      Human myelin basic protein (cys21) (scd1nm).
KW      Myelin basic protein MBP. MBP-X2Cys-81: predicted protein; P110.
KW      Multiple sclerosis; autoimmune disease; diagnosis; therapy.
KW      T-lymphocyte; T-cell; anergy; apoptosis.
OS      Homo sapiens.
Key
  Location/Qualifiers
  FT      60..85
  FT      /label= X2
  FT      /note= "exon 2-extended region"
  misc_difference 81
  /note= "Cys-81 may be replaced by any standard amino acid, esp. an uncharged amino acid of mol wt below below about 150, for the Ser, in constructs of the invention"
  EN      W05634522-A1.
  PR      07-NOV-1996.
  PR      22-APR-1996; 005611.
  PR      02-MAY-1995; US-431648.
  PR      02-MAY-1995; US-431644.
  PR      07-JUN-1995; US-482114.
  PA      (ALEX-) ALEXION PHARM INC.
  PA      (USSH.) US DEPT HEALTH & HUMAN SERVICES.
  PA      Leonardo MJ, Melis L, McFarland HF, Mueller EE, Mueller JF,
  PA      Nye SR, Polley GM, Spindler SP, Wilkins JA;
  PA      WPI; 96-50689/50.
  DE      N-PDB: 1A1899.
  FT      New human myelin basic protein and proteolipid protein variants)
  PT      used in the assessment, diagnosis and treatment of multiple
  PT      sclerosis.
  CS      Claim 1, Page 79-80, 15pp; English.
  CC      The native human 210 kDa myelin basic protein (W03117) of myelin basic
  CC      protein, MBP-X2Cys-81, includes an exon 2-extended region (X2) that
  CC      may contain an epitope involved in the pathogenesis of multiple
  CC      sclerosis (MS). The X2 region is not found in the MBP of healthy
  CC      adults. Recombinant MBP-X2, or variants modified to improve
  CC      bacterial expression (see also W0407), can be produced in a
  CC      large scale in bacterial hosts. They are useful for assessing
  CC      T-cells for responsiveness to MBP epitopes and can be used as
  CC      therapeutic agents that act by inducing T cell responses,
  CC      including anergy and apoptosis, as a means of treating MS.
  CC      Sequence 197 AA;
  CY      1 MYKDS 5
  CY      11111
  CP      83 MYKDS 97
  RESULT  12
  ID      W06107
  ID      W06107 standard: Protein; 203 AA.
  DT      01-FEB-1997 (first entry)
  DI      P0624: myelin basic protein MBP-X2Cys81; bact.
  KW      Myelin basic protein MBP. MBP-X2Cys-81: predicted protein; P110.
  KW      Multiple sclerosis; autoimmune disease; diagnosis; therapy.
  KW      T-lymphocyte; T-cell; anergy; apoptosis.
  OS      Synthetic.
  Key
  Location/Qualifiers
  FT      60..85
  FT      /label= X2
  FT      /note= "exon 2-extended region"
  misc_difference 81
  /note= "Cys-81 may be replaced by any standard amino acid, esp. an uncharged amino acid of mol wt below below about 150, for the Ser, in constructs of the invention"
  EN      W05634522-A1.
  PR      07-NOV-1996.
  PR      22-APR-1996; 005611.
  PR      02-MAY-1995; US-431648.
  PR      02-MAY-1995; US-431644.
  PR      07-JUN-1995; US-482114.
  PA      (ALEX-) ALEXION PHARM INC.
  PA      (USSH.) US DEPT HEALTH & HUMAN SERVICES.
  PA      Leonardo MJ, Melis L, McFarland HF, Mueller EE, Mueller JF,
  PA      Nye SR, Polley GM, Spindler SP, Wilkins JA;
  PA      WPI; 96-50689/50.
  DE      N-PDB: 1A1899.
  FT      New human myelin basic protein and proteolipid protein variants)
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  CS      Claim 1, Page 79-80, 15pp; English.
  CC      The native human 210 kDa myelin basic protein (W03117) of myelin basic
  CC      protein, MBP-X2Cys-81, includes an exon 2-extended region (X2) that
  CC      may contain an epitope involved in the pathogenesis of multiple
  CC      sclerosis (MS). The X2 region is not found in the MBP of healthy
  CC      adults. Recombinant MBP-X2, or variants modified to improve
  CC      bacterial expression (see also W0407), can be produced in a
  CC      large scale in bacterial hosts. They are useful for assessing
  CC      T-cells for responsiveness to MBP epitopes and can be used as
  CC      therapeutic agents that act by inducing T cell responses,
  CC      including anergy and apoptosis, as a means of treating MS.
  CC      Sequence 197 AA;
  CY      1 MYKDS 5
  CY      11111
  CP      83 MYKDS 97
  RESULT  12
  ID      W06107
  ID      W06107 standard: Protein; 203 AA.
  DT      01-FEB-1997 (first entry)
  DI      P0624: myelin basic protein MBP-X2Cys81; bact.
  KW      Myelin basic protein MBP. MBP-X2Cys-81: predicted protein; P110.
  KW      Multiple sclerosis; autoimmune disease; diagnosis; therapy.
  KW      T-lymphocyte; T-cell; anergy; apoptosis.
  OS      Synthetic.
  Key
  Location/Qualifiers
  FT      60..85
  FT      /label= X2
  FT      /note= "exon 2-extended region"
  misc_difference 81
  /note= "Cys-81 may be replaced by any standard amino acid, esp. an uncharged amino acid of mol wt below below about 150, for the Ser, in constructs of the invention"
  EN      W05634522-A1.
  PR      07-NOV-1996.
  PR      22-APR-1996; 005611.
  PR      02-MAY-1995; US-431648.
  PR      02-MAY-1995; US-431644.
  PR      07-JUN-1995; US-482114.
  PA      (ALEX-) ALEXION PHARM INC.
  PA      (USSH.) US DEPT HEALTH & HUMAN SERVICES.
  PA      Leonardo MJ, Melis L, McFarland HF, Mueller EE, Mueller JF,
  PA      Nye SR, Polley GM, Spindler SP, Wilkins JA;
  PA      WPI; 96-50689/50.
  DE      N-PDB: 1A1899.
  FT      New human myelin basic protein and proteolipid protein variants)
  PT      used in the assessment, diagnosis and treatment of multiple
  PT      sclerosis.
  CS      Claim 1, Page 79-80, 15pp; English.
  CC      The native human 210 kDa myelin basic protein (W03117) of myelin basic
  CC      protein, MBP-X2Cys-81, includes an exon 2-extended region (X2) that
  CC      may contain an epitope involved in the pathogenesis of multiple
  CC      sclerosis (MS). The X2 region is not found in the MBP of healthy
  CC      adults. Recombinant MBP-X2, or variants modified to improve
  CC      bacterial expression (see also W0407), can be produced in a
  CC      large scale in bacterial hosts. They are useful for assessing
  CC      T-cells for responsiveness to MBP epitopes and can be used as
  CC      therapeutic agents that act by inducing T cell responses,
  CC      including anergy and apoptosis, as a means of treating MS.
  CC      Sequence 197 AA;
  CY      1 MYKDS 5
  CY      11111
  CP      83 MYKDS 97
  RESULT  12
  ID      W06107
  ID      W06107 standard: Protein; 203 AA.
  DT      01-FEB-1997 (first entry)
  DI      P0624: myelin basic protein MBP-X2Cys81; bact.
  KW      Myelin basic protein MBP. MBP-X2Cys-81: predicted protein; P110.
  KW      Multiple sclerosis; autoimmune disease; diagnosis; therapy.
  KW      T-lymphocyte; T-cell; anergy; apoptosis.
  OS      Synthetic.
  Key
  Location/Qualifiers
  FT      60..85
  FT      /label= X2
  FT      /note= "exon 2-extended region"
  misc_difference 81
  /note= "Cys-81 may be replaced by any standard amino acid, esp. an uncharged amino acid of mol wt below below about 150, for the Ser, in constructs of the invention"
  EN      W05634522-A1.
  PR      07-NOV-1996.
  PR      22-APR-1996; 005611.
  PR      02-MAY-1995; US-431648.
  PR      02-MAY-1995; US-431644.
  PR      07-JUN-1995; US-482114.
  PA      (ALEX-) ALEXION PHARM INC.
  PA      (USSH.) US DEPT HEALTH & HUMAN SERVICES.
  PA      Leonardo MJ, Melis L, McFarland HF, Mueller EE, Mueller JF,
  PA      Nye SR, Polley GM, Spindler SP, Wilkins JA;
  PA      WPI; 96-50689/50.
  DE      N-PDB: 1A1899.
  FT      New human myelin basic protein and proteolipid protein variants)
  PT      used in the assessment, diagnosis and treatment of multiple
  PT      sclerosis.
  CS      Claim 1, Page 79-80, 15pp; English.
  CC      The native human 210 kDa myelin basic protein (W03117) of myelin basic
  CC      protein, MBP-X2Cys-81, includes an exon 2-extended region (X2) that
  CC      may contain an epitope involved in the pathogenesis of multiple
  CC      sclerosis (MS). The X2 region is not found in the MBP of healthy
  CC      adults. Recombinant MBP-X2, or variants modified to improve
  CC      bacterial expression (see also W0407), can be produced in a
  CC      large scale in bacterial hosts. They are useful for assessing
  CC      T-cells for responsiveness to MBP epitopes and can be used as
  CC      therapeutic agents that act by inducing T cell responses,
  CC      including anergy and apoptosis, as a means of treating MS.
  CC      Sequence 197 AA;
  CY      1 MYKDS 5
  CY      11111
  CP      83 MYKDS 97
  RESULT  12
  ID      W06107
  ID      W06107 standard: Protein; 203 AA.
  DT      01-FEB-1997 (first entry)
  DI      P0624: myelin basic protein MBP-X2Cys81; bact.
  KW      Myelin basic protein MBP. MBP-X2Cys-81: predicted protein; P110.
  KW      Multiple sclerosis; autoimmune disease; diagnosis; therapy.
  KW      T-lymphocyte; T-cell; anergy; apoptosis.
  OS      Synthetic.
  Key
  Location/Qualifiers
  FT      60..85
  FT      /label= X2
  FT      /note= "exon 2-extended region"
  misc_difference 81
  /note= "Cys-81 may be replaced by any standard amino acid, esp. an uncharged amino acid of mol wt below below about 150, for the Ser, in constructs of the invention"
  EN      W05634522-A1.
  PR      07-NOV-1996.
  PR      22-APR-1996; 005611.
  PR      02-MAY-1995; US-431648.
  PR      02-MAY-1995; US-431644.
  PR      07-JUN-1995; US-482114.
  PA      (ALEX-) ALEXION PHARM INC.
  PA      (USSH.) US DEPT HEALTH & HUMAN SERVICES.
  PA      Leonardo MJ, Melis L, McFarland HF, Mueller EE, Mueller JF,
  PA      Nye SR, Polley GM, Spindler SP, Wilkins JA;
  PA      WPI; 96-50689/50.
  DE      N-PDB: 1A1899.
  FT      New human myelin basic protein and proteolipid protein variants)
  PT      used in the assessment, diagnosis and treatment of multiple
  PT      sclerosis.
  CS      Claim 1, Page 79-80, 15pp; English.
  CC      The native human 210 kDa myelin basic protein (W03117) of myelin basic
  CC      protein, MBP-X2Cys-81, includes an exon 2-extended region (X2) that
  CC      may contain an epitope involved in the pathogenesis of multiple
  CC      sclerosis (MS). The X2 region is not found in the MBP of healthy
  CC      adults. Recombinant MBP-X2, or variants modified to improve
  CC      bacterial expression (see also W0407), can be produced in a
  CC      large scale in bacterial hosts. They are useful for assessing
  CC      T-cells for responsiveness to MBP epitopes and can be used as
  CC      therapeutic agents that act by inducing T cell responses,
  CC      including anergy and apoptosis, as a means of treating MS.
  CC      Sequence 197 AA;
  CY      1 MYKDS 5
  CY      11111
  CP      83 MYKDS 97
  RESULT  12
  ID      W06107
  ID      W06107 standard: Protein; 203 AA.
  DT      01-FEB-1997 (first entry)
  DI      P0624: myelin basic protein MBP-X2Cys81; bact.
  KW      Myelin basic protein MBP. MBP-X2Cys-81: predicted protein; P110.
  KW      Multiple sclerosis; autoimmune disease; diagnosis
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FI 004-1-XC
 FI W0631501-1
 PR 07-NOV-1996
 PD 22-APR-1996
 PE 02-MAY-1995
 PR 02-MAY-1995
 PR 07-JUN-1996
 EA (ALBA) ALFAXION PHARM INC
 PA (USSH) US FTFT HEALTH & HUMAN SERVICES
 PI Lennarz MT, Malle L, McFarland HF, Mueller EE, Mueller JP
 PI Nye SH, Pelletier CM, Squinto SP, Wilkins JA
 DR WPI: 96-508996/50
 DR NIDep: 141836
 PT New human myelin basic protein and proteolipid protein variant(s) -
 PT used in the assessment, diagnosis and treatment of multiple
 PT sclerosis
 PS Disclosure: Page 81-82; 156pp; English.
 CC A 21.5 kDa foetal isoform (W063107) of myelin basic protein,
 CC MBP-X2Cys81/bact, is the product of a DNA construct (T41846)
 CC based on the human foetal MBP-X2Cys81 isoform (W06399) but
 CC utilising bacterially-preferred codons in place of the native human
 CC codons (see also T41883). This increases prodn. of the MBP in E.
 CC coli by at least 1000 fold. Recombinant MBP 21.5 Polypeptides (see also
 CC W06399 and W06108) are useful in the clinical assessment, diagnosis
 CC and treatment of MS.
 SQ Sequence 203 AA:
 QY 1 MYKUS 5
 DB 83 MYKUS 87
 Query Match 100.0% Score 27 DB 1, Length 203
 Best Local Similarity 100.0% Pred. No. 21:
 Matches 5 Conservative 0 Mismatches 0 Indels 0 Gaps 0
 RESULT 13
 W06108
 ID W06108 standard: Protein: 203 AA
 AC W06108
 DE 01-FEB-1997 (first entry)
 DE F-441 myelin basic protein MBP-X2Cys81/bact.
 KM Myelin basic protein, MBP, MBP-X2Cys81, proteolipid protein; ELP,
 KM Multiple sclerosis; autoimmune disease; diagnosis; therapy;
 KM Tryptophan, Tryptic, tryptic, tryptics.
 OS Synthesis
 FH FTY
 FI region
 FI 60-85
 FI 60-85
 FI /note: "exon 2-encoded region, with Cys81ser
 FI mutation"
 FI 196, 203
 FI peptide
 FI /label: Hexa-histidine-tag
 FI /note: "the hexa-histidine tag facilitates
 FI purification of the recombinant protein
 FI from host cells"
 PN W0633622-A1
 PD 07-NOV-1996
 PE 22-APR-1996
 PR 02-MAY-1995
 PR 02-MAY-1995
 PR 07-JUN-1996
 PA (ALBA) ALFAXION PHARM INC
 PA (USSH) US FTFT HEALTH & HUMAN SERVICES
 PI Lennarz MT, Malle L, McFarland HF, Mueller EE, Mueller JP
 PI Nye SH, Pelletier CM, Squinto SP, Wilkins JA
 DR WPI: 96-508996/50
 DR NIDep: 141837
 PT New human myelin basic protein and proteolipid protein variant(s)
 PT used in the assessment, diagnosis and treatment of multiple
 PT sclerosis

FS Disclosure: Page 82-83; 156pp; English.
 CC A 21.5 kDa foetal isoform (W06108) of myelin basic protein,
 CC MBP-X2Cys81/bact, is the product of a DNA construct (T41846)
 CC based on the human foetal MBP-X2Cys81 isoform (W06399) but
 CC utilising codons that are highly expressed in bacterial genes in
 CC place of the native codons (see also T41883) and incorporating a
 CC sequence coding for a hexa-histidine tail. This allows large-
 CC scale prodn. and purification of the MBP in bacterial hosts.
 CC Recombinant MBP 21.5 Polypeptides (see also W06399 and W06107) are
 CC useful in the clinical assessment, diagnosis and treatment of MS.
 SQ Sequence 203 AA:
 QY 1 MYKUS 5
 DB 50 MYKUS 54
 Query Match 100.0% Score 27 DB 1, Length 157
 Best Local Similarity 100.0% Pred. No. 16:
 Matches 5 Conservative 0 Mismatches 0 Indels 0 Gaps 0
 RESULT 14
 W24262
 ID W24262 standard: Protein: 157 AA.
 AC W24262
 DE 15-OCT-1997 (first entry)
 DE Murine protein for induction of interferon-gamma.
 KM Interferon-gamma, immunocompetent cell, malignant tumour;
 KM Viral disease; bacterial infection; immune disease.
 OS Mus musculus.
 FH Key
 FI misc_difference 70
 FI /note: "Encoded by AYT"
 FI J09157180-A
 PD 17-JUN-1997
 PE 24-JAN-1996
 PR 04-OCT-1995
 PR 10-MAR-1995
 PR 29-SEP-1995
 PA (HAYR) HAYASHIWARA SEIROTSU KAKAKU
 TR WPI: 97-469491/34
 DR N-PSDB: T80210
 DE A d123 containing a polypeptide which induces interferon-gamma -
 DE useful for treating e.g. malignant tumours, viral, bacterial or
 DE immune diseases
 PS Disclosure: Page 10-11; 12pp; Japanese.
 CC This sequence represents a protein which induces interferon-gamma
 CC production in immunocompetent cells. This protein may be used as
 CC the major component in a drug for the prevention and treatment of
 CC e.g. malignant tumours, viral diseases, bacterial infections and
 CC immune diseases.
 SQ Sequence 157 AA:
 QY 1 MYKUS 5
 DB 50 MYKUS 54
 Query Match 100.0% Score 27 DB 1, Length 157
 Best Local Similarity 100.0% Pred. No. 16:
 Matches 5 Conservative 0 Mismatches 0 Indels 0 Gaps 0
 RESULT 15
 W24258
 ID W24258 standard: Protein: 157 AA.
 AC W24258
 DE 15-OCT-1997 (first entry)
 DE Human protein for induction of interferon-gamma.
 KM Interferon-gamma, immunocompetent cell; malignant tumour;
 KM Viral disease; bacterial infection; immune disease.
 OS Homo sapiens.

C:Genetics:
A:MAP Position: 11E
C:Keywords: Nucleotide Protein

Query Match 88.9% Score 27 DB 2 Length 143
Best Local Similarity 100.0% Pred No 22
Matches 4: Conservative 0 Mismatches 0 Indels 0 Gaps 0

CY 1 MYKDS 5
DB 329 MYKDS 72

RESULT 8
S60224
C:Species: Mus musculus (house mouse)
C:Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 10-Sep-1997
C:Accession: S60226
R:Okamura, H.; Tsuboi, H.; Komatsu, T.; Yutsudo, M.; Haku, A.; Tamimoto, T.; Toriue,
Nature 378, 88-91, 1995
A:Title: Cloning of a new cytokine that induces IFN-gamma production by T cells.
A:Reference number: S60226
A:Accession: S60226
A:Status: Preliminary
A:Molecule type: mRNA
A:Peptides: 1192 (KKA)
A:Cross-references: PDB: 24949 MID: 91064822 PIR: J1909319 PIR: 91064822

Query Match 100.0% Score 27 DB 2 Length 193
Best Local Similarity 100.0% Pred No 15
Matches 5: Conservative 0 Mismatches 0 Indels 0 Gaps 0

CY 1 MYKDS 5
DB 85 MYKDS 42

RESULT 9
XND00
C:Species: Dictyostelium discoideum
C:Alternate names: glucose-1-phosphate uridylyltransferase; UDPglucose pyrophosphorylase
C:Species: Dictyostelium discoideum
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 05-Sep-1997
R:Kachib, J.A.; Dettin, R.P.
Nucleic Acids Res 15, 3891-3906, 1987
A:Title: Structure and sequence of a GCF glucose-1-phosphorylase gene of Dictyostelium
A:Reference number: S07363 MID: 87211075
A:Accession: S07363
A:Molecule type: DNA
A:Peptides: 1311 (KAG)
A:Cross-references: EMBL: Y00145; MID: 97384; PIR: 97385
C:Comments: This enzyme catalyzes alpha-D-glucose-1-phosphate and nucleoside triphosphate
C:Genetics:
A:Introns: 1671-1711, 1713
A:Superfamily: uridylyltransferase
C:Keywords: nucleotidyltransferase

Query Match 88.9% Score 24 DB 1 Length 511
Best Local Similarity 88.9% Pred No 36-02
Matches 4: Conservative 1 Mismatches 0 Indels 0 Gaps 0

CY 1 MYKDS 5
DB 200 MYKDS 212

RESULT 10

A24050
C:Species: Mus musculus (house mouse)
C:Date: 12-Jul-1997 #sequence_revision 06-Jul-1997 #text_change 19-Jun-1998
C:Accession: A24050
R:Baras, I.W.; Levinson, P.B.; Brady, M.; Williams, S.R.; Martin, D.; D.N.
J Biol Chem 272, 3415-3422, 1995
A:Reference number: A24051 MID: 92217721
A:Accession: A24050
A:Molecule type: mRNA
A:Peptides: 1792 (CAR)
A:Superfamily: herpovirus ribonucleoside-diphosphate reductase large chain
C:Keywords: DNA replication, oxidoreductase

Query Match 88.9% Score 24 DB 2 Length 722
Best Local Similarity 88.9% Pred No 36-02
Matches 4: Conservative 1 Mismatches 0 Indels 0 Gaps 0

CY 1 MYKDS 5
DB 406 LYKDS 410

RESULT 11
S14807
C:Species: Schistosoma mansoni
C:Date: 31-Dec-1994 #sequence_revision 11-Dec-1994 #text_change 15-Sep-1997
R:Sarabia, M.J.F.; McInerney, C.; Harris, P.; Gordon, C.; Fantes, P.
Mol. Gen. Genet. 229, 241-251, 1993
A:Title: The cdc22 gene encodes a protein that is essential for the development of the fluke Schistosoma mansoni.
A:Reference number: S14807
A:Accession: S14807
A:Molecule type: DNA
A:Peptides: 1811 (SAF)
A:Cross-references: EMBL: X67110; MID: 927446; PIR: 927447
C:Genetics:
A:Gene: cdc22
A:Introns: 7/1
C:Superfamily: herpovirus ribonucleoside-diphosphate reductase large chain
C:Keywords: DNA replication, oxidoreductase

Query Match 88.9% Score 24 DB 2 Length 511
Best Local Similarity 88.9% Pred No 36-02
Matches 4: Conservative 1 Mismatches 0 Indels 0 Gaps 0

CY 1 MYKDS 5
DB 400 LYKDS 410

RESULT 12
B48687
C:Species: Plasmodium falciparum
C:Date: 09-May-1994 #sequence_revision 09-May-1994 #text_change 21-May-1995
R:Roblin, R.; Salem, J.S.; Li, L.S.; Yang, F.; Muma, S.; Ward, L.; Fisher, A.; Bannan,
Proc Natl Acad Sci USA 90, 2460-2464, 1993
A:Title: Cloning, sequence determination, and regulation of the ribonucleotide reductase
A:Reference number: A48687
A:Accession: B48687
A:Status: Preliminary
A:Molecule type: DNA
A:Peptides: 1824 (PCE)
A:Cross-references: PIR: 93077; MID: 931791; PIR: 931792
C:Comments: This gene encodes the ribonucleoside-diphosphate reductase large chain
C:Keywords: herpovirus ribonucleoside-diphosphate reductase large chain
R:217-443 700-802/Dictyostelium discoideum reductase large chain predicted
R:217-443/Dictyostelium discoideum reductase large chain predicted

GenCore version 4.5
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QM Protein : protein search using sw model

Run on : June 22, 1999 10:56:43 : Search time 45.16 seconds

(without alignments)
2,972 Million cell updates/sec

Title : US-09-030-061-4

Perfect score : 27

Sequence : 1 MYKDS 5

Scoring table : BLOSUM62

Searched : 74019 seqs, 26840295 residues

Database : SwissProt_36.1

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	27	100.0	1431_ENTHI	P42648 entamoeba h
2	27	100.0	1431_ENTHI	P28268 borrelia b
3	27	100.0	1431_ENTHI	059465 helicobacte
4	27	100.0	1431_ENTHI	014116 homo sapien
5	27	100.0	1431_ENTHI	P70380 mus musculu
6	27	100.0	1431_ENTHI	019073 sus scrofa
7	27	100.0	1431_ENTHI	P97636 ratu
8	27	100.0	1431_ENTHI	P02685 homo sapien
9	27	100.0	1431_ENTHI	P04370 mus musculu
10	27	100.0	1431_ENTHI	P22905 mus musculu
11	27	100.0	1431_ENTHI	P04094 ratu
12	27	100.0	1431_ENTHI	P48786 petroselinu
13	27	100.0	1431_ENTHI	P36148 saccharomyc
14	27	100.0	1431_ENTHI	P22662 methanococc
15	27	100.0	1431_ENTHI	052063 pseudomonas
16	27	100.0	1431_ENTHI	P37700 clostridium
17	27	100.0	1431_ENTHI	059934 streptococc
18	27	100.0	1431_ENTHI	P23821 homo sapien
19	27	100.0	1431_ENTHI	P07422 mus musculu
20	27	100.0	1431_ENTHI	P50647 plasmodium
21	27	100.0	1431_ENTHI	P50647 plasmodium
22	27	100.0	1431_ENTHI	P36602 schistosach
23	27	100.0	1431_ENTHI	002775 saccharomyc
24	27	100.0	1431_ENTHI	P18102 diatomella
25	27	100.0	1431_ENTHI	P08800 dictyostell
26	27	100.0	1431_ENTHI	P18948 caenobacteri
27	27	100.0	1431_ENTHI	P54722 bacillus su
28	27	100.0	1431_ENTHI	P53442 saccharomyc
29	27	100.0	1431_ENTHI	P34146 saccharomyc
30	27	100.0	1431_ENTHI	P48839 vidio sp.
31	27	100.0	1431_ENTHI	P16445 plasmodium
32	27	100.0	1431_ENTHI	P13824 plasmodium
33	27	100.0	1431_ENTHI	P13824 plasmodium
34	27	100.0	1431_ENTHI	P54986 dictyostell
35	27	100.0	1431_ENTHI	P37126 xanthomonas
36	27	100.0	1431_ENTHI	001116 homo sapien
37	27	100.0	1431_ENTHI	P27895 saccharomyc
38	27	100.0	1431_ENTHI	P40145 homo sapien
39	27	100.0	1431_ENTHI	P97490 mus musculu
40	27	100.0	1431_ENTHI	P40146 ratu
41	27	100.0	1431_ENTHI	P40136 bacillus an
42	27	100.0	1431_ENTHI	049163 methanococc
43	27	100.0	1431_ENTHI	P39482 bacillus me

ALIGNMENTS

44	27	95.2	13	1	DR02_BACSU
45	27	95.2	13	1	DR02_BACSU
RESULT 1					
1431_ENTHI	1431_ENTHI	STANDARD	PRI	239 AA	
AC	P42648				
DT	01-NOV-1995 (REL. 32, CREATED)				
DT	01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)				
DT	01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)				
DE	14-3-3 PROTEIN I (14-3-3-1)				
OS	ENTAMOeba HISTOLYTICA				
OC	EUKARYOTA: PROTISTA: SARCOMASTICOPHYTES: SARCOMASTICOPHYTES: ENTAMOEBIDIA				
LN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN:HM-1:IMSS				
PA	SAMUELSON T, SHEN P, MCKELER G, DESOTEAUX S, GU R, TORIA A				
PE	SEQUENCE (AUG-1-94) IS EM-2/SEMPAN/1431 DATA BANKS.				
CC	1 - SIMILARITY: BELONGS TO THE 14-3-3 FAMILY.				
DE	EMBL: U13418; G571361; 1431.1				
DR	PROSITE: PS00796; 1433.2; 1				
DR	PROSITE: PS00797; 1433.2; 1				
KM	MULTIGENE FAMILY.				
SC	SEQUENCE 143 AA; 27339 MW; P0460856 CPO220				
RESULT 2					
DNAX_BORBU	DNAX_BORBU	STANDARD	PRI	635 AA	
IT	P28608				
AC	P28608				
DT	01-DEC-1994 (REL. 24, CREATED)				
DT	01-DEC-1994 (REL. 24, LAST SEQUENCE UPDATE)				
DT	01-DEC-1994 (REL. 24, LAST ANNOTATION UPDATE)				
DE	DNAX PROTEIN (HEAT SHOCK PROTEIN 70) (HSP-70).				
GN	DNAX				
OS	ROPERETIA FRIGIDIFRONTI (LYME DISEASE SPIROCHETE).				
OC	PROKARYOTA: GRAM-NEGATIVE: SPIROCHETES: SPIROCHETES: SPIROCHETES				
OC	SPIROCHAETACEAE				
LN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN:ISLATE CAL2				
PA	MEDLINE: 92363568				
PE	ANCOJA T, CHET P, STERNE G, CATWYLER F, STRECHER D				
SA	LANESNA F, FLETCHER G				
EL	INFECT IMMUN: 60:3704-3713(1992).				
LN	[2]				
RP	SEQUENCE FROM N.A.				
RC	MEDLINE: 92363568				
PA	THIRY F, HANSEN P, CAMPELLE T, OETHEIMER G, J				
EL	M. MED. 111: 111-112(1993).				
LN	[3]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN:257				
PA	MEDLINE: 93014208				
RA	WALLICH F, HELMES C, SCHABERLE U, LOBET Y, MOTER S, E				
PA	KRAMER M D, SIMON M M				
EL	INFECT IMMUN: 60:4856-4864(1992).				
CC	1 - FUNCTION: ACTS AS A CHAPERONE (BY SIMILARITY).				
CC	1 - INDUCTION: BY HEAT SHOCK.				


```

QY      1 MYKDS 5
      |||||
Db      328 MYKDS 332

RESULT  14

Query Match
Host Local Similarity 100.0% 100.0% Score 271 DB 1: Length 1088
Matches 51 Conservative 0 Mismatches 0 Indels 0 Gaps 0

QY      1 MYKDS 5
      |||||
Db      750 MYKDS 754

RESULT  13
YK47_YEAST
ID      YK47_YEAST STANDARD PRG: 743 AA.
AC      P36148;
DT      01-JUN-1994 (REL. 29, CREATED)
DT      01-JUN-1994 (REL. 29, LAST SEQUENCE UPDATE)
DT      01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
DE      HYPOTHEICAL 83.6 KD PROTEIN IN COP1-MET1 INTERGENIC REGION.
GN      YK067M.
OS      SACTARACMYCES TEREVISIAE (BAKERY'S YEAST).
OC      EUBACTERIA: FUNGI: ASCOMYCOTINA: HEMIASCOMYCETES.
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN-S288C;
RA      VAN VILIEF-FREDRIK J.C., PLANTA R.J.;
SV      SUBMITTED (MAR-1994) TO EMBL/GENBANK/DBJ DATA BANKS.
CC      SPROTEINIAL ACIDIC, INTEGRAL MEMBRANE PROTEIN (PROBABLE).
CC      -1- SIMILARITY: STRONG TO YEAST YK011W.
QY      1- SIMILARITY: STRONG TO YEAST YK011W.
QY      EMBL: Z22972, GI865372.
QY      PIR: S38143; S38143.
KW      HYPOTHETICAL PROTEIN; TRANSMEMBRANE.
FT      TRANSMEM 31 55 POTENTIAL.
FT      TRANSMEM 46 85 POTENTIAL.
FT      TRANSMEM 502 524 POTENTIAL.
FT      TRANSMEM 539 555 POTENTIAL.
FT      TRANSMEM 743 AA. 501-41 MM. (PDBVAL) CHECKED.

Query Match
Host Local Similarity 100.0% 100.0% Score 473 DB 1: Length 743
Matches 51 Conservative 0 Mismatches 0 Indels 0 Gaps 0

```

Job time: 71 sec

ATPA_ME1BA
 ID ATPA_ME1BA STANDARD: PRT: 578 AA.
 AC P22662;
 DT 01-AUG-1991 (REL. 19, CREATED)
 DT 01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)
 DT 01-MAY-1992 (REL. 22, LAST ANNOTATION UPDATE)
 DE ATP SYNTHASE ALPHA CHAIN (EC 3.6.1.34).
 GN ATPA.
 OS METHANOCALOPTIMA PARKERI.
 CC ARCHAEOTA; BACTERIA; EUBACTERIA; METHANOMITOTRICHIALES; METHANOSARCINACEAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 83291829.
 RA YANOWITZ K.L., EYA S., MAEDA M., PUTAI M.,
 RL J. BIOL. CHEM. 264:10954-10959(1989).
 CC THIS IS A CATALYTIC SUBUNIT.
 CC -1- SIMILARITY: STRONG TO OTHER ARCHAEACTERIA ALPHA SUBUNITS, ALSO
 CC RELATED TO THE BETA SUBUNITS OF FO-F1 ATPASES.
 DR EMBL: J04836; G149820; -.
 DR PIR: A34293; A34283.
 DR PROSITE: PS00152: ATPASE ALPHA BETA 1.
 KW ATP SYNTHESIS; HYDROGEN ION TRANSPORT; HYDROLASE; ATP-BINDING.
 FT M_91ND 228 235 ATP (BY SIMILARITY).
 SQ SEQUENCE 578 AA: 54638 MW: 441647 CPO32;

Query Match 88.9%; Score 24; DB 1; Length 578;
 Best Local Similarity 80.0%; Pred. No. 1,6e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MYKDS 5
 DB 430 LYKDS 434

RESULT 15
 ATZC_PSESD
 ID ATZC_PSESD STANDARD: PRT: 403 AA.
 AC 052063;
 DT 15-JUL-1998 (REL. 36, CREATED)
 DT 15-JUL-1998 (REL. 36, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE N-ISOPROPYLAMMELITE ISOPROPYL AMIDHYDROLASE (EC 3.5.1.-).
 GN ATZC.
 OS PSEUDOMONAS SP. (STRAIN ADP).
 CC PERKARIOTA; SPACILITRICES; STYLOBACTERIA; AERUBIC BUDS AND COCOON;
 CC PSEUDOMONADACEAE.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 98083069.
 RA SADOWSKY M.T., TONG Z., DE SOUZA M., WACKETT L.F.,
 RL J. BACTERIOL. 180:152-158(1998).
 CC FUNCTION: TRANSFORMS N-ISOPROPYLAMMELITE TO CYANURIC ACID AND
 CC ISOPROPYLAMINE.
 CC -1- PATHWAY: THIRD STEP IN AIRALINE DEGRADATION PATHWAY.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).
 CC -1- SIMILARITY: BELONGS TO THE N-ACTYL-D-AMINO-ACID DEACYLASE FAMILY.
 DE EMBL: AF017572; G2736101; -.
 KW HYDROLASE.
 SQ SEQUENCE 403 AA: 41938 MW: 39909081 CPO32;

Query Match 88.9%; Score 24; DB 1; Length 403;
 Best Local Similarity 80.0%; Pred. No. 1,1e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MYKDS 5
 DB 267 LYKDS 271

Search completed: June 22, 1999, 10:59:45



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OM profile: 100000 search, 1000000000

Run on: June 22, 1999, 11:01:22 Search time 93.17 seconds

(without alignments)
3 417 Million cell updates/sec

File: us-09-030-061-4

Perfect score: 27

Sequence: 1 MYRS R

Scoring table: 180763 segs, 55169189 residues

Database:

SPTREMBL_8:*

- 1: sp_fungi:*
- 2: sp_human:*
- 3: sp_invertebrate:*
- 4: sp_mammal:*
- 5: sp_mhc:*
- 6: sp_oranella:*
- 7: sp_phase:*
- 8: sp_plant:*
- 9: sp_bacteria:*
- 10: sp_podentia:*
- 11: sp_virus:*
- 12: sp_vertebrate:*
- 13: sp_unclassified:*
- 14: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	PF	ID	Description
1	27	100.0	193	2	075599	075599 homo sapien
2	27	100.0	175	1	023830	023830 jacobsen
3	27	100.0	194	10	023834	023834 jacobsen
4	24	99.9	175	1	012513	012513 saccharomy
5	24	99.9	172	1	013807	013807 schistosom
6	24	99.9	211	1	060026	060026 heliomyces
7	24	99.9	206	2	075602	075602 homo sapien
8	24	99.9	197	3	017598	017598 caenorhabdi
9	24	88.9	197	3	018137	018137 caenorhabdi
10	24	88.9	161	3	045176	045176 caenorhabdi
11	24	88.9	84	3	017062	017062 anopheles
12	24	88.9	45	3	016845	016845 drosophila
13	24	88.9	97	3	023792	023792 drosophila
14	24	82.3	87	3	013137	013137 drosophila
15	24	88.6	246	6	060652	060652 acidiopsis
16	24	88.6	404	6	060762	060762 acidiopsis
17	24	88.6	450	6	060906	060906 mycoplasma
18	24	99.9	106	6	023827	023827 mycoplasma
19	24	99.9	106	6	023827	023827 mycoplasma
20	24	99.9	445	6	075139	075139 mycoplasma
21	24	88.6	219	3	023139	023139 bacillus su
22	24	88.6	74	3	060907	060907 mycoplasma
23	24	88.6	117	4	060907	060907 mycoplasma
24	24	88.6	253	10	023834	023834 mus muscula
25	24	88.6	253	10	023834	023834 mus muscula
26	24	88.6	117	10	070826	070826 mus muscula
27	24	88.6	504	19	060103	060103 mus muscula
28	24	88.6	1112	19	097872	097872 mus muscula
29	24	88.6	924	11	060108	060108 unknown

ALIGNMENTS

RESULT	1	PRELIMINARY:	PR: 193 AA.
ID	075599		
AC	075599		
LI	01-NV-1998 (REMBL_08, CREATED)		
DT	01-NV-1998 (REMBL_08, LAST SEQUENCE UPDATE)		
DE	01-NV-1998 (REMBL_08, LAST ANNOTATION UPDATE)		
GN	INTERLEUKIN-18 PRECURSOR.		
OS	HOMO SAPIENS (HUMAN)		
OC	PRIMATES, CATARRHINI, HOMINIDAE, HOMO.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
FA	YONG D. GUIN D., LIHO H., HAITAO W.		
RT	Cloning and sequencing of the cDNA for precursor hIL-18.		
RL	Submitted (Oct. 1998) to EMBL/GENBANK/DBJ DATA BANKS.		
DR	EMBL: AF077611; G348071; .		
KW	SIGNAL.		
FT	SIGNAL 1 36	POTENTIAL:	
FT	CHAIN 37 193	INTERLEUKIN-18.	
SC	SEQUENCE 193 AA; 22324 MW; 85000033 CR222;		
Query Match	100.0%	Score 27: DB 2: Length 193:	
Footprint	100.0%	Pred. No. 21:	
Matches	2: Conservative	0: Mismatches	0: Indels
27	1 MYRS 5		
28	87 MYRS 91		
RESULT	2	PRELIMINARY:	PR: 1758 AA.
ID	023830		
AC	023830		
LI	01-NV-1998 (REMBL_01, CREATED)		
DT	01-NV-1998 (REMBL_01, LAST SEQUENCE UPDATE)		
DE	01-NV-1998 (REMBL_01, LAST ANNOTATION UPDATE)		
GN	TRANSCRIPTION FACTOR.		
OS	CARINORHINUS ELEGANS.		
OC	PRIMATES, CATARRHINI, HOMINIDAE, HOMO.		
RN	[1]		
RP	SEQUENCE FROM N.A.		
FA	YONG D. GUIN D., LIHO H., HAITAO W.		
RT	Cloning and sequencing of the cDNA for precursor hIL-18.		
RL	Submitted (Oct. 1998) to EMBL/GENBANK/DBJ DATA BANKS.		
DR	EMBL: AF077611; G348071; .		
KW	SIGNAL.		
FT	SIGNAL 1 36	POTENTIAL:	
FT	CHAIN 37 193	INTERLEUKIN-18.	
SC	SEQUENCE 193 AA; 22324 MW; 85000033 CR222;		
Query Match	100.0%	Score 27: DB 2: Length 193:	
Footprint	100.0%	Pred. No. 21:	
Matches	2: Conservative	0: Mismatches	0: Indels
27	1 MYRS 5		
28	87 MYRS 91		

[illegible]

```

Query Match: 86.9% SCORE 24; DB 1; Length 1072;
Best Local Similarity 80.0%; Pred. NO. 7.4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Hits
CY 1 MYKDS 5
      ||||
Db 188 LYKDS 192

RESULT 6
000026
12 000026 FELINISAMY FET 211 AA.
AC 000026;
D1 01-NOV-1996 (MEMM1991 01 CREATED)
D1 01-NOV-1996 (TEPM1991 01 LAST SEQUENCE UPDATE)
D1 01-AUG-1996 (TEPM1991 02 LAST ANNOUNCEMENT UPDATE)
15 TMMINDEFECTIVE CLONE GR17.

```

OS AFFLOWCES CAPSULATUS
 OC ENKARYOTA PROTISTASCA MYCOTA FUNGOMYCETES ELETOMYCETES ONYGENALES
 OC ONYGENALES AFFLOWCES
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN-02126
 RA CHANTASHEFF P. JEFFIS K.C. WELLS J. KAWAYASHI S.
 RL SUBMITTED (MAY-1995) TO EMBL/GENBANK/NCBI DATA BANKS.
 DR EMBL: 021268 G881332
 SQ SEQUENCE 311 AA 23906 MW: 0989A960 CRC32:

Query Match 86.94 Score 241 15.11 Length 311
 Best Local Similarity 86.94 Prog No 139-002
 Matches 4: Conservative 1: Mismatches 0: Indels 0: Gaps 0:

QY 1 MYKDS 5
 DB 153 LYKDS 157

RESULT 7
 ID 075603 PRELIMINARY: PRT: 506 AA.
 AC 075603
 DT 01-NOV-1998 (TREMEREEL 08, CREATED)
 DT 01-NOV-1998 (TREMEREEL 08, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMEREEL 08, LAST ANNOTATION UPDATE)
 DE GLIAL CELLS MISSING PROTEIN HOMOLOG
 OS HOMO SAPIENS (HUMAN)
 OC ENKARYOTA METAZOA CHEDATA VERTEBRATA MAMMALIA EUTHERIA
 OC PRIMATES CATARRHINI HOMININAE HOMO
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN:
 RA PAPERBYA V. HERAFA S. CHENISHT J. TROMATO S. MERT K. MATSUMURA H.
 RA YAMASAKI M. FUSUKI S. ARITA N.
 RT "Molecular cloning of a human brain homologue of glial cells missing
 RT (hscmb)."
 RL SUBMITTED (MAY 1998) TO EMBL/GENBANK/NCBI DATA BANKS
 DR EMBL: AF090600 G851283
 SQ SEQUENCE 506 AA 11987 MW: 4198773 TRF32:

Query Match 89.39 Score 241 15.11 Length 506
 Best Local Similarity 89.39 Prog No 24-002
 Matches 4: Conservative 1: Mismatches 0: Indels 0: Gaps 0:

QY 1 MYKDS 5
 DB 291 LYKDS 295

RESULT 8
 ID 017598 PRELIMINARY: PRT: 561 AA
 AC 017598
 DT 01-JAN-1999 (TREMEREEL 05, CREATED)
 DT 01-JAN-1999 (TREMEREEL 05, LAST SEQUENCE UPDATE)
 DT 01-JAN-1999 (TREMEREEL 05, LAST ANNOTATION UPDATE)
 DE C2527.5
 OS CAENOPHABDITIS ELEGANS
 OC ENKARYOTA METAZOA NEMATODA SEPTENTRIVIA PHABDITIA PHABDITIA
 OC PHABDITIA PHABDITIDAE PHABDITIDAE PHABDITIDAE CAENOPHABDITIS
 RN (1)
 RP SEQUENCE FROM N.A.
 RA MEDLINE: 94154718
 RA WILSON R. ALANSON R. ANDERSON K. BAYNES C. BEPES M. BONFIELD J.
 RA BERT N. CONNEL M. COOPER J. JOHNSON A. OXATON M.
 RA DEAR S. DE Z. DUBREIN P. FAVIOL A. FULTON I. GARDNER A. GREEN P.
 RA HAKINS T. HILLIER I. JEFF M. JOHNSON L. JONES M. KERSHAW J.
 RA KIPREN T. LAISER N. LATREILLE P. LIGHTNING J. LLOYD C.
 RA KOPORAI A. MORTIMER R. O'CALLAGHAN M. PARSONS J. PERCY G.

RA KIPREN I. POOPRA A. SAUNDERS D. SHOWNKEEN R. SMITHON N. SMITH A.
 RA SUNKHAMER R. STAN P. STEVEN J. THIPPY-WHEATON J. WHEATON J.
 RA VAUDIN M. VAUGHAN K. WATSON P. WATSON A. WEINSTOCK L.
 RA WILKINSON-SEFOAT J. WILKINSON-SEFOAT J. WILKINSON-SEFOAT J.
 RT "2 ME of 101268 G881332"
 RT elegans
 RL NATURE 368:33-38(1994)
 DR EMBL: Z81059 G530174
 SQ SEQUENCE 301 AA 40455 MW: 950B1290 CRC32:

Query Match 88.94 Score 241 15.11 Length 301
 Best Local Similarity 88.94 Prog No 239-002
 Matches 4: Conservative 1: Mismatches 0: Indels 0: Gaps 0:

QY 1 MYKDS 5
 DB 188 MYKDS 192

RESULT 9
 ID 018337 PRELIMINARY: PRT: 197 AA.
 AC 018337
 DT 01-NOV-1998 (TREMEREEL 01, CREATED)
 DT 01-NOV-1998 (TREMEREEL 01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1998 (TREMEREEL 08, LAST ANNOTATION UPDATE)
 DE COSMID C31H1.
 GN C31H1.2
 OS CAENOPHABDITIS ELEGANS
 OC ENKARYOTA METAZOA NEMATODA SEPTENTRIVIA PHABDITIA PHABDITIA
 OC PHABDITIA PHABDITIDAE PHABDITIDAE PHABDITIDAE CAENOPHABDITIS
 RN (1)
 RP SEQUENCE FROM N.A.
 RA MEDLINE: 94150718
 RA WILSON R. ALANSON R. ANDERSON K. BAYNES C. BEPES M. BONFIELD J.
 RA BERT N. CONNEL M. COOPER J. JOHNSON A. OXATON M.
 RA DEAR S. DE Z. DUBREIN P. FAVIOL A. FULTON I. GARDNER A. GREEN P.
 RA HAKINS T. HILLIER I. JEFF M. JOHNSON L. JONES M. KERSHAW J.
 RA KIPREN T. LAISER N. LATREILLE P. LIGHTNING J. LLOYD C.
 RA MCMURRAY A. MORTIMER R. O'CALLAGHAN M. PARSONS J. PERCY G.
 RA FERRIN L. FERRIN L. FERRIN L. FERRIN L. FERRIN L.
 RA SUNKHAMER R. STAN P. STEVEN J. THIPPY-WHEATON J. WHEATON J.
 RA VAUDIN M. VAUGHAN K. WATSON P. WATSON A. WEINSTOCK L.
 RA WILKINSON-SEFOAT J. WILKINSON-SEFOAT J. WILKINSON-SEFOAT J.
 RT "2 ME of 101268 G881332"
 RT elegans
 RL NATURE 368:33-38(1994)
 DR EMBL: Z81059 G530174
 SQ SEQUENCE 301 AA 40455 MW: 950B1290 CRC32:

Query Match 88.94 Score 241 15.11 Length 197
 Best Local Similarity 88.94 Prog No 139-002
 Matches 4: Conservative 1: Mismatches 0: Indels 0: Gaps 0:

QY 1 MYKDS 5
 DB 131 LYKDS 135

RESULT 10
 ID 045176 PRELIMINARY: PRT: 1651 AA.
 AC 045176

[illegible]

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OY      1 MYRS 5
        :||||
Db      168 LYRS 172

Search completed: June 22, 1990, 11:01:23
Job time: 169 sec

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GenCore version 4.5
Copyright (c) 1993-1998 Compuser Ltd

OM protein - protein search using sw model

Run on: June 22, 1999, 10:58:48 : Search time 61.51 seconds

(without alignments)
3.045 Million cell updates/sec

Title: US-09-030-061-5

Perfect score: 26

Sequence: 1 STLSO 5

Scoring table:

42000002

Search:

110739 seqs, 2760001 residues

Database:

PIR-58**

1: p1r1**
2: p1r2**
3: p1r3**
4: p1r4**

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No	Query Match	Length	CP	IT	Description
1	26	100.0	915	1	MMBEV3
2	25	100.0	802	1	UGBCPP
3	24	100.0	784	1	UGBCPP
4	24	100.0	772	1	UGBCPP
5	24	100.0	772	1	UGBCPP
6	24	100.0	772	1	UGBCPP
7	24	100.0	772	1	UGBCPP
8	24	100.0	772	1	UGBCPP
9	24	100.0	772	1	UGBCPP
10	24	100.0	772	1	UGBCPP
11	24	100.0	772	1	UGBCPP
12	24	100.0	772	1	UGBCPP
13	24	100.0	772	1	UGBCPP
14	24	100.0	772	1	UGBCPP
15	24	100.0	772	1	UGBCPP
16	24	100.0	772	1	UGBCPP
17	24	100.0	772	1	UGBCPP
18	24	100.0	772	1	UGBCPP
19	24	100.0	772	1	UGBCPP
20	24	100.0	772	1	UGBCPP
21	24	100.0	772	1	UGBCPP
22	24	100.0	772	1	UGBCPP
23	24	100.0	772	1	UGBCPP
24	24	100.0	772	1	UGBCPP
25	24	100.0	772	1	UGBCPP
26	24	100.0	772	1	UGBCPP
27	24	100.0	772	1	UGBCPP
28	24	100.0	772	1	UGBCPP
29	24	100.0	772	1	UGBCPP
30	24	100.0	772	1	UGBCPP
31	24	100.0	772	1	UGBCPP
32	24	100.0	772	1	UGBCPP
33	24	100.0	772	1	UGBCPP
34	24	100.0	772	1	UGBCPP
35	24	100.0	772	1	UGBCPP
36	24	100.0	772	1	UGBCPP
37	24	100.0	772	1	UGBCPP
38	24	100.0	772	1	UGBCPP
39	24	100.0	772	1	UGBCPP

40	23	88.5	120	1	K3HUNT
41	23	88.5	100	1	K3HUNT
42	23	88.5	100	1	K3HUNT
43	23	88.5	100	1	K3HUNT
44	23	88.5	100	1	K3HUNT
45	23	88.5	100	1	K3HUNT

ALIGNMENTS

RESULT 1

MMBEV3

ribonucleoside diphosphate reductase (EC 1.17.4.1) large chain - human cytomegalovirus

Alternate names: ribonucleoside reductase large chain, O15 protein

Species: human cytomegalovirus, human herpesvirus 5

Accession: S09808

Accession: S09808

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Accession: S09808

Accession: S09808

Accession: S09808

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Accession: S09808

Accession: S09808

A:Molecule type: mRNA
 A:Residues: 1-964 <ASP>
 A:Cross-references: 158 M16601, M167460, P1D:q407166
 C:Genetics:
 A:Gene: sfp, M16
 A:Map position: 4931-4931 M167460
 A:Map position: 4931-4931
 C:Superfamily: unassigned eta-related proteins; eta transforming protein homology
 C:Keywords: DNA binding, transcription regulation, zinc finger
 F:661/661/Domain: eta finger
 F:662/662/Domain: eta finger
 F:663/663/Domain: eta finger
 F:664/664/Domain: eta finger
 F:665/665/Domain: eta finger

Query Match: 100.0%, Score 26, DB 2, Length 984,
 Best Local Similarity: 100.0%, Prod. No. 25002,
 Matches 5, Conservative 0, Mismatches 0, Indels 0, Gaps 0

QY 1 STISC 5
 Db 1487 STISC 1491

RESULT 7
 A23475
 G surface protein - Parametium primurella (SGCS)
 C:Species: Parametium primurella
 C:Date: 21-Mar-1999 #seqtype=transcript 21 Mar-1999 #seqtype=change 21-Dec-1999
 C:Accession: A23475
 R:Patel, A., Kallio, M., Caron, F., Meyer, E.,
 J. Mol. Biol. 189, 47-60, 1985
 A:Title: Nucleotide sequence of the Parametium primurella G surface protein. A huge pro
 A:Reference number: A23475, M167460, P1D:q407166
 A:Accession: A23475
 A:Molecule type: DNA
 A:Residues: 1-2718 <PRN>
 A:Note: The authors translated the codon TGC for residue 2665 as Trp
 C:Genetics:
 A:Genetic code: SGCS
 C:Superfamily: G surface protein

Query Match: 100.0%, Score 26, DB 2, Length 2718,
 Best Local Similarity: 100.0%, Prod. No. 58002,
 Matches 5, Conservative 0, Mismatches 0, Indels 0, Gaps 0

QY 1 STISC 5
 Db 1487 STISC 1491

RESULT 8
 S10220
 Sodium/proline symporter - Salmonella typhimurium
 A:Cross-references: 158 M16601, M167460, P1D:q407166
 C:Genetics:
 A:Gene: sfp, M16
 A:Map position: 4931-4931 M167460
 A:Map position: 4931-4931
 C:Superfamily: unassigned eta-related proteins; eta transforming protein homology
 C:Keywords: DNA binding, transcription regulation, zinc finger
 F:661/661/Domain: eta finger
 F:662/662/Domain: eta finger
 F:663/663/Domain: eta finger
 F:664/664/Domain: eta finger
 F:665/665/Domain: eta finger

Query Match: 100.0%, Score 26, DB 2, Length 2718,
 Best Local Similarity: 100.0%, Prod. No. 58002,
 Matches 5, Conservative 0, Mismatches 0, Indels 0, Gaps 0

QY 1 STISC 5
 Db 1487 STISC 1491

RESULT 9
 J02382
 Sodium/proline symporter - Pseudomonas fluorescens
 N:Alternate names: proline permease
 C:Species: Pseudomonas fluorescens
 C:Date: 20-Feb-1999 #seqtype=transcript 20-Feb-1999 #seqtype=change 13-Sep-1999
 C:Accession: J02382
 R:Hosoya, H., Nakamura, K.,
 Biosci. Biotechnol. Biochem. 63, 2229-2231, 1994
 A:Title: DNA sequence of proline permease gene from Pseudomonas and predicted structu
 A:Reference number: J02382
 A:Accession: J02382
 A:Molecule type: DNA
 A:Residues: 1-494 <HOS>
 C:Function:
 A:Superfamily: eta-related proteins; eta transforming protein homology
 C:Keywords: proline transporter, sodium transport, symport system, transmembrane protei
 F:2-56/Domain: transmembrane #status predicted <TM>
 F:4-6-73/Domain: transmembrane #status predicted <TM>
 F:128-147/Domain: transmembrane #status predicted <TM>
 F:163-185/Domain: transmembrane #status predicted <TM>
 F:191-210/Domain: transmembrane #status predicted <TM>
 F:234-257/Domain: transmembrane #status predicted <TM>
 F:274-297/Domain: transmembrane #status predicted <TM>
 F:317-339/Domain: transmembrane #status predicted <TM>
 F:372-395/Domain: transmembrane #status predicted <TM>
 F:429-444/Domain: transmembrane #status predicted <TM>
 F:455-473/Domain: transmembrane #status predicted <TM>

Query Match: 100.0%, Score 26, DB 2, Length 102,
 Best Local Similarity: 100.0%, Prod. No. 15002,
 Matches 5, Conservative 0, Mismatches 0, Indels 0, Gaps 0

QY 1 STISC 5
 Db 340 STISC 344

RESULT 9
 J02382
 Sodium/proline symporter - Pseudomonas fluorescens
 N:Alternate names: proline permease
 C:Species: Pseudomonas fluorescens
 C:Date: 20-Feb-1999 #seqtype=transcript 20-Feb-1999 #seqtype=change 13-Sep-1999
 C:Accession: J02382
 R:Hosoya, H., Nakamura, K.,
 Biosci. Biotechnol. Biochem. 63, 2229-2231, 1994
 A:Title: DNA sequence of proline permease gene from Pseudomonas and predicted structu
 A:Reference number: J02382
 A:Accession: J02382
 A:Molecule type: DNA
 A:Residues: 1-494 <HOS>
 C:Function:
 A:Superfamily: eta-related proteins; eta transforming protein homology
 C:Keywords: proline transporter, sodium transport, symport system, transmembrane protei
 F:2-56/Domain: transmembrane #status predicted <TM>
 F:4-6-73/Domain: transmembrane #status predicted <TM>
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 F:274-297/Domain: transmembrane #status predicted <TM>
 F:317-339/Domain: transmembrane #status predicted <TM>
 F:372-395/Domain: transmembrane #status predicted <TM>
 F:429-444/Domain: transmembrane #status predicted <TM>
 F:455-473/Domain: transmembrane #status predicted <TM>

1. Change 13-Sep-1998
 2. ext #
 3. revision 04-Dec-1992
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 6. equivalents (Nomenclature)
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 261. not

Adv. Polym. Sci., 1991, 100, 1-16.
 V. J. Fraser, C. M. Smith, H. O. Venter, J. C. Attille: White-stemmed rabbit sequencing and assembly of *Haemophilus influenzae* Rd.

A:Reference number: A64000: MIP:4545930
A:Accession: H64148
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1113 of 1188
A:Date: 13-Sep-1998
A:Note: best homolog was a hypothetical protein from Escherichia coli

Query Match: 100.0% Score 26, DB 2, Length 113;
Best Local Similarity: 100.0%; Pred. No. 44;
Matches: 51 Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 1 STISC 5
DB 17 STISC 21

RESULT 15

E71484
Probable GMP kinase: Chlamydia trachomatis (serotype D, strain UW3/Cx)
C:Species: Chlamydia trachomatis
C:Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 13-Sep-1998
C:Accession: E71484

R:Stephens, R.S.; Kaiman, S.; Lammel, C.F.; Fan, J.; Marathe, P.; Aravind, L.; Mitchell, submitted to Genbank, May 1998

A:Description: Genbank sequence of an obligate intracellular pathogen of humans: Chlamydia

A:Reference number: A71460

A:Accession: E71484

A:Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-245 <ARN>

A:Cross-reference: GP:AE001728, GP:AE001723, NID:J3322126, PID:G3329130

A:Experimental source: serotype D, strain UW-3/Cx

C:Genetics:

A:Gene: pyrH

Query Match: 100.0% Score 26, DB 2, Length 245;
Best Local Similarity: 100.0%; Pred. No. 82;
Matches: 51 Conservative 0, Mismatches 0, Indels 0, Gaps 0;

QY 1 STISC 5
DB 105 STISC 109

Search completed: June 22, 1999, 10:58:50
Job time: 149 sec



GenCore version 4.5
Copyright (c) 1993 - 1998 CompuGen Ltd.

OM protein - protein search using a model

Run on: June 22, 1999, 10:44:39 : Search time 61.72 seconds

(without alignments)
1.648 Million cell updates/sec

Title: US-09-030-061-5

Perfect score: 26

Sequence: 1 STS25

Scoring table: ELCSUM62

Scanned: 10000 seqs 2000000 residues

Database: A.geneseq_34.*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is printed by multiples of 100. Score distribution.

SUMMARIES

Result No	Score	Query Match	Length	DP	ID	Description
1	26	100.0	984	1	P80927	Sequence of the hu
2	26	100.0	984	1	P80927	Human PH-20 protol
3	26	100.0	984	1	P80927	Human PH-20 protol
4	26	100.0	984	1	P80927	Human PH-20 (deriv
5	26	100.0	984	1	P80927	Human PH-20 (deriv
6	26	100.0	984	1	P80927	Human PH-20 (deriv
7	26	100.0	984	1	P80927	Human PH-20 (deriv
8	26	100.0	984	1	P80927	Human PH-20 (deriv
9	26	100.0	984	1	P80927	Human PH-20 (deriv
10	26	100.0	984	1	P80927	Human PH-20 (deriv
11	26	100.0	984	1	P80927	Human PH-20 (deriv
12	26	100.0	984	1	P80927	Human PH-20 (deriv
13	26	100.0	984	1	P80927	Human PH-20 (deriv
14	26	100.0	984	1	P80927	Human PH-20 (deriv
15	26	100.0	984	1	P80927	Human PH-20 (deriv
16	26	100.0	984	1	P80927	Human PH-20 (deriv
17	26	100.0	984	1	P80927	Human PH-20 (deriv
18	26	100.0	984	1	P80927	Human PH-20 (deriv
19	26	100.0	984	1	P80927	Human PH-20 (deriv
20	26	100.0	984	1	P80927	Human PH-20 (deriv
21	26	100.0	984	1	P80927	Human PH-20 (deriv
22	26	100.0	984	1	P80927	Human PH-20 (deriv
23	26	100.0	984	1	P80927	Human PH-20 (deriv
24	26	100.0	984	1	P80927	Human PH-20 (deriv
25	26	100.0	984	1	P80927	Human PH-20 (deriv
26	26	100.0	984	1	P80927	Human PH-20 (deriv
27	26	100.0	984	1	P80927	Human PH-20 (deriv
28	26	100.0	984	1	P80927	Human PH-20 (deriv
29	26	100.0	984	1	P80927	Human PH-20 (deriv
30	26	100.0	984	1	P80927	Human PH-20 (deriv
31	26	100.0	984	1	P80927	Human PH-20 (deriv
32	26	100.0	984	1	P80927	Human PH-20 (deriv
33	26	100.0	984	1	P80927	Human PH-20 (deriv
34	26	100.0	984	1	P80927	Human PH-20 (deriv
35	26	100.0	984	1	P80927	Human PH-20 (deriv
36	26	100.0	984	1	P80927	Human PH-20 (deriv
37	26	100.0	984	1	P80927	Human PH-20 (deriv
38	26	100.0	984	1	P80927	Human PH-20 (deriv
39	26	100.0	984	1	P80927	Human PH-20 (deriv
40	26	100.0	984	1	P80927	Human PH-20 (deriv
41	26	100.0	984	1	P80927	Human PH-20 (deriv
42	26	100.0	984	1	P80927	Human PH-20 (deriv
43	26	100.0	984	1	P80927	Human PH-20 (deriv

ALIGNMENTS

RESULT 1
P80927
ID P80927 standard; protein; 984 AA.
AC P80927;
DE 29-DEC-1990 (first entry)
DE Sequence of the human placental choriocarcinoma (HPL) receptor (HMR)
KW Human receptor; ligand-binding; transcription activation
OS Homo sapiens.
PN M08803168-A.
PD 05-MAY-1988.
PF 23-OCT-1987; 052732.
PR 20-OCT-1987; US-108471.
PA (SAUK) Salk Inst for Biol Stud.
PI Evans RM, Weinberger CA, Hollenberg SM, Giguere V.
DI WPI88-13242/19.
DR N-TER: N0920.
FT 5x Multiple CNA coding for hormone receptors -
FT comprising glucocorticoid, mineralocorticoid, thyroid hormone
PT and novel hormone receptors
PS Claim 17; Fig IV-2(B)-1 and -2; 243p; English.
CC DNAs encoding hormone receptors and the hormone receptors themselves are
CC claimed. The HMR can be used to make the hormone receptor proteins and
CC functional modified forms in quantities not previously possible. The
CC receptor proteins can be used to screen cDNA libraries for receptor agonists or
CC antagonists. They can also be used in diagnostic assays.
SQ Sequence 984 AA:

Query: M08803168-A (100%) Score: 26 ID: P80927 (984)
Size: 984 (100%) Score: 26 ID: P80927 (984)
Matches: 984 (100%) Conserved: 0 Mismatches: 0 Indels: 0 Gaps: 0
DB 100 STS25 100
OR 1 STS25 5
AC 2
DE 29-DEC-1990 (first entry)
DE Sequence of the human placental choriocarcinoma (HPL) receptor (HMR)
KW Human receptor; ligand-binding; transcription activation
OS Homo sapiens.
PN M08803168-A.
PD 05-MAY-1988.
PF 23-OCT-1987; 052732.
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PA (SAUK) Salk Inst for Biol Stud.
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FT 5x Multiple CNA coding for hormone receptors -
FT comprising glucocorticoid, mineralocorticoid, thyroid hormone
PT and novel hormone receptors
PS Claim 17; Fig IV-2(B)-1 and -2; 243p; English.
CC DNAs encoding hormone receptors and the hormone receptors themselves are
CC claimed. The HMR can be used to make the hormone receptor proteins and
CC functional modified forms in quantities not previously possible. The
CC receptor proteins can be used to screen cDNA libraries for receptor agonists or
CC antagonists. They can also be used in diagnostic assays.
SQ Sequence 984 AA:

1. H_2SO_4 is a strong acid.

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      100% Match      100.0%      Score: 26, 281, Length: 503,
      100% Ident. Similarity: 100.0%      Pred. No. 4.6e+02;
      0.0% Mismatches      0.0% Indels      0.0% Gaps

```

THE

FI peptide from sperm surface protein which stimulates antibody
 PT prodn.
 PS Example 4: Fig 4: 79pp: English.
 CC Sperm surface proteins of peptides stimulate an immune response to
 CC produce antibodies with block sperm-egg fusion and provide
 CC contraception pref sperm surface proteins are: the p11-20 and p8-8
 CC Sperm surface proteins.
 SO Sequence 509 AA.

A ^a	P _{AN-15} ^b	(100% + 0.0%)
B ^c	H ₂ O ₂ -PH-	100%+10 HLB ₆

Year	1969	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1969	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

[illegible]

the presence of a 5' cap (Mullish, 1980). The sequence is that of a 6'-terminal fragment of human sperm surface protein P1, a glycoprotein which can be used in a contraceptive vaccine (Mullish, 1980).

the H18 sequence, the new method is as effective or more effective than the other methods. The new method is more convenient. The sequence of the H18 gene is identical to that of the partial sequence of the H18 gene, which is 206 bp (numbered based on H18 sequence).

Country	Malaysia	Year	1996	Score	20	DB	1	Length	275
Field No.	115	Sex	♂	Wing	100.00	Prod. No.	250002		
Month	5	Month/day	05/05/96	Weight	0	Age	0	Stage	0

1. **Introduction**
 2. **Methodology**
 3. **Results**
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RM PH α 1-antitrypsin deficiency; sperm surface proteins

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the N and O atoms.

Db 439 STLS: 443

RESULT	5
R47349	
ID	R47349 standard; Protein; 275 AA
AC	R47349;

05 Home sapiens.

12-JUN-1962; U

PT Contraceptive vaccine for reducing sperm-egg fusion - comprises peptide from sperm surface protein which stimulates an antibody

CC Sperm surface proteins of peptides stimulate an immune response to
CC produce antibodies which block sperm-egg fusion and provide
CC contraception. Pref. sperm surface proteins are the pN-2 and pN-3

Query Match

Matches	0	Conservative	0	Misstatements	0	Indoors	0	Outdoors	0
0Y	1	STASC	5						

RESULT	6
R65216	

DE P-selectin.

AM alicornio, italiano, 1970-1980
OS Homo sapiens.
IN W09506118-A.
PD 02-MAR-1995.

PA (OKLA) UNIV OKLAHOMA STATE
PI McEever RP, Pan J;
OR WPT; 95-106847/14.

11 Treat of p... with viral disease, malignancies and immune
12 factors
13 Example A... (p265) Induces Interferon-gamma (IFN-gamma)
14 ... By ... (p265) Its sequence was deduced from
15 ... (p265) isolated from a mouse liver library.
16 ... (p265) Interferon protein can be produced in high yields
17 ... (p265) cop. Interferon protein, transformed with a vector
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11 MISC_difference 140
12 /Label: R1401
13 /Note: "Wild type Arg is replaced by His"
14
15 W0972441-A1.
16 10-JUL-1997.
17 20-DEC-1997: W22047.
18 29-DEC-1995: US-580667.
19 (INCY-) INCYTE PHARM INC.
20 Cooke PG, Coleman R, Hawkins PR,
21 WPI: 97-363677/33.
22 N-PSDB: T74988.
23
24 Novel Interferon gamma inducing factor 2 - used to screen for
25 compounds to diagnose, treat or prevent tissue damage associated
26 with inflammation
27
28 Claim 3: Page 1: 60pp: English.
29
30 This protein sequence represents an Interferon gamma inducing factor 2
31 (IGIF-2) variant, identified from a liver cDNA library. This sequence
32 differs from IGIF-2 identified from a T-lymphocyte cDNA library (W22047)
33 in that amino acid 140 is found to be changed from Asn to His. A second
34 variant, W22047, also exists. Probe derived from the IGIF-2 cDNA
35 sequences can be used to quantify the expression of IGIF-2 in conditions
36 that are associated with inflammation or aberrant expression of IGIF-2.
37 The protein can be used to screen for compounds that interact with
38 IGIF-2, such as antibodies, antagonists or other ligands. Specifically,
39 ribozymes or antisense sequences of IGIF-2 expression or a cellular
40 protein can also be used to diagnose, prevent or treat IGIF-2 induction
41 of proliferation, differentiation or maturation of leukocytes or
42 lymphocytes, especially in relation to tissue damage associated
43 with inflammation.
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45 Note: This sequence does not appear in the specification. It has
46 been made by substituting the IGIF-2 sequence presented in W22047.
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48 Sequence 193 AA:
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100

CC Information of activity. The protein can also be used to diagnose, prevent
 CC or treat HIV-2 infection of proliferation, differentiation or maturation
 CC of leukocytes or lymphocytes, especially in relation to tissue damage
 CC associated with inflammation
 CC Sequence 193 AA:

Query Match 100.0% Score 26; DB 1; Length 193;
 Best Local Similarity 100.0% Pred No 1 4e-02

Matches 0; Conservative 0; Mismatches 0; Indels 0; Gaps 0

OY 1 STISC 5
 DB 108 STISC 112

RESULT 13
 W15704
 ID W15704 standard; peptide: 193 AA

AC W15704

DI 26 JAN-1998 (first entry)

DE Mouse interferon-gamma inducer protein.

KM Interferon-gamma, IFN-gamma; antiviral; antitoxic; radiotherapy;

KW Immunoregulatory; antitumor agent; chemotherapy; leukopenia;

KW Chemotherapy; immunocompetent cells; asthma; hay fever;

KW Rheumatism; Interleukin-1 killer cell

OS Mus musculus.

FT Key Location/Qualifiers

FI Misc-differences 70

PI EP-76779-A1

PN 09-APR-1997

PT 26-SEP-1997

PR 26-SEP-1997

PR 26-SEP-1997

PR 26-SEP-1997

PR 26-SEP-1997

PR 26-SEP-1997

PR 26-SEP-1997

PR 26-SEP-1997

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PR 26-SEP-1997

PR 26-SEP-1997

PR 26-SEP-1997

PR 26-SEP-1997

PR 26-SEP-1997

PR 26-SEP-1997

PR 26-SEP-1997

AC W15704
 DI 01-APR-1998 (first entry)
 DE Peptide sequence #4 displayed by RSW17 monoclonal phages.
 KM Peptide immunogen; vaccination; allergy; epidermis; immune response;
 KM Immunoglobulin E; antibody RSW17; antigen; RSW17; RSW17; RSW17;
 KM antibody; mast cells; basophil; immunisation; monoclonal phage; circular;
 OS Synthetic.

OS Homo sapiens.

FT Key Location/Qualifiers

FI Key Location/Qualifiers

FI Key Location/Qualifiers

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FI Key Location/Qualifiers

Genome version 4.5
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OM protein - protein search, using SW model

Run on: June 23, 1999 11:01:27 Search time 23.17 Seconds
(without alignments)
3,317 Million cell updates/sec

Title: US-09-030-061-5
Perfect score: 26
Sequence: 1 stlvs
Sequencing Lab: Bioscience

Searched: 190763 seqs, 55169189 residues

Database: SPTRMBL_8:

1: sp_fungi:
2: sp_human:
3: sp_invertebrate:
4: sp_mammal:
5: sp_rhiz:
6: sp_cyanobact:
7: sp_plant:
8: sp_bacteria:
9: sp_bacteria:
10: sp_bacteria:
11: sp_virus:
12: sp_viribact:
13: sp_unclassified:
14: sp_archaea:

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by methods of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	100.0	984	1	007454 saccharomy
2	26	100.0	488	2	013787 homo sapien
3	26	100.0	193	2	005509
4	26	100.0	747	3	009586 caenorhabd
5	26	100.0	233	3	003238 caenorhabd
6	26	100.0	332	3	016644 caenorhabd
7	26	100.0	446	3	018276 caenorhabd
8	26	100.0	489	9	047551 escherichia
9	26	100.0	489	9	047552 escherichia
10	26	100.0	488	3	047553 escherichia
11	26	100.0	489	9	053255 rickettsia
12	26	100.0	488	9	054978 salmonella
13	26	100.0	489	9	054979 salmonella
14	26	100.0	489	9	054980 salmonella
15	26	100.0	489	9	054981 salmonella
16	26	100.0	489	9	054982 salmonella
17	26	100.0	489	9	054983 salmonella
18	26	100.0	489	9	054984 salmonella
19	26	100.0	489	9	054985 salmonella
20	26	100.0	489	9	054986 salmonella
21	26	100.0	489	9	054987 salmonella
22	26	100.0	489	9	054988 salmonella
23	26	100.0	489	9	054989 salmonella
24	26	100.0	489	9	054990 salmonella
25	26	100.0	489	9	054991 salmonella
26	26	100.0	489	9	054992 salmonella
27	26	100.0	489	9	054993 salmonella
28	26	100.0	489	9	054994 salmonella
29	26	100.0	489	9	054995 salmonella
30	26	100.0	489	9	054996 salmonella

ALIGNMENTS

Result	ID	Query Match	Score	DB ID	Length	Prod. No.	Matches	Mismatches	Gaps
1	007454	PRELIMINARY	PRT: 984 AA						
2	013787	FREDIMINARY	PRT: 4560 AA						
3	013787	FREDIMINARY	PRT: 4560 AA						
4	013787	FREDIMINARY	PRT: 4560 AA						
5	013787	FREDIMINARY	PRT: 4560 AA						
6	013787	FREDIMINARY	PRT: 4560 AA						
7	013787	FREDIMINARY	PRT: 4560 AA						
8	013787	FREDIMINARY	PRT: 4560 AA						
9	013787	FREDIMINARY	PRT: 4560 AA						
10	013787	FREDIMINARY	PRT: 4560 AA						
11	013787	FREDIMINARY	PRT: 4560 AA						
12	013787	FREDIMINARY	PRT: 4560 AA						
13	013787	FREDIMINARY	PRT: 4560 AA						
14	013787	FREDIMINARY	PRT: 4560 AA						
15	013787	FREDIMINARY	PRT: 4560 AA						
16	013787	FREDIMINARY	PRT: 4560 AA						
17	013787	FREDIMINARY	PRT: 4560 AA						
18	013787	FREDIMINARY	PRT: 4560 AA						
19	013787	FREDIMINARY	PRT: 4560 AA						
20	013787	FREDIMINARY	PRT: 4560 AA						
21	013787	FREDIMINARY	PRT: 4560 AA						
22	013787	FREDIMINARY	PRT: 4560 AA						
23	013787	FREDIMINARY	PRT: 4560 AA						
24	013787	FREDIMINARY	PRT: 4560 AA						
25	013787	FREDIMINARY	PRT: 4560 AA						
26	013787	FREDIMINARY	PRT: 4560 AA						
27	013787	FREDIMINARY	PRT: 4560 AA						
28	013787	FREDIMINARY	PRT: 4560 AA						
29	013787	FREDIMINARY	PRT: 4560 AA						
30	013787	FREDIMINARY	PRT: 4560 AA						

100.0% STISC 5 DB 31 Length 747 AA
 Best Local Similarity 100.0% Pred. No. 256-02
 Matches 51 Conservative 0 Mismatches 0 Indels 0 Gaps 0
 DB 555 STISC 559
 RESULT 5
 ID 093238 PRELIMINARY PRT 325 AA
 AC 093238
 DT 01-FEB-1997 (TREMURIEL 02, CREATED)
 DI 01-FEB-1997 (TREMURIEL 02, LAST SEQUENCE UPDATE)
 DE C17G1.4
 OS CAENORHABDITIS ELEGANS
 CC EUDARVOTA: METAZOA: NEMATODA: SEPERENTHEA: PHARODITIA: PHARODITIAE
 CC PHARODITIA: PHARODITIAE: PHARODITIAE: PHARODITIAE: PHARODITIAE: PHARODITIAE
 RN [1]
 RP SEQUENCE FROM N.A.
 RL WHITE S.
 RI SUBMITTED (NOV-1996) TO EMBL/GENBANK/DBJ DATA BANKS
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 94150718
 RA WILSON J., AINSWORTH P., ANDERSON K., RAYNES C., PIPPS M., BRINLEY J.,
 RA BURTON J., CONNELL M., COOPER J., COOPER J., CRATTON M.,
 RA LEAF S., LEAF S., HERRIN P., HAVILL A., HUTTON J., JACOBIA A., JELLY P.,
 RA HAWKING T., HILLIER L., JIER M., JOHNSTON L., JONES M., KERSHAW J.,
 RA KIRSTEN I., LAISTER N., LAIBELLE P., LIGHTNING J., LLOYD J.,
 RA MCMURRAY A., MORTIMER R., O'CALLAGHAN M., PARKS N., PERRY C.,
 RA RIVEN L., PETERA A., SAUNDERS E., SHAWKLER B., SHAWKLER B., SMITH A.,
 RA SAUNDHAMMER P., STADEN B., STURTON J., THIRLEY W., THIRLEY W., THIRLEY W.,
 RA WILKINSON-SPROAT J., WOLDMAN P.
 FT * 2 3 ME 35 5 nucleotide sequence from chromosome 11 of C.
 RT elegans.
 RL NATURE 368:32-38(1994).
 DR EMBL: Z78415; E259012;
 SO SEQUENCE 925 AA; 99340 MW; C78CA124 CDS;

100.0% STISC 5 DB 31 Length 747 AA
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 RA KIRSTEN I., LAISTER N., LAIBELLE P., LIGHTNING J., LLOYD J.,
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 SO SEQUENCE 925 AA; 99340 MW; C78CA124 CDS;

100.0% STISC 5 DB 31 Length 747 AA
 Best Local Similarity 100.0% Pred. No. 256-02
 Matches 51 Conservative 0 Mismatches 0 Indels 0 Gaps 0
 DB 555 STISC 559
 RESULT 5
 ID 093238 PRELIMINARY PRT 325 AA
 AC 093238
 DT 01-FEB-1997 (TREMURIEL 02, CREATED)
 DI 01-FEB-1997 (TREMURIEL 02, LAST SEQUENCE UPDATE)
 DE C17G1.4
 OS CAENORHABDITIS ELEGANS
 CC EUDARVOTA: METAZOA: NEMATODA: SEPERENTHEA: PHARODITIA: PHARODITIAE
 CC PHARODITIA: PHARODITIAE: PHARODITIAE: PHARODITIAE: PHARODITIAE: PHARODITIAE
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 RP SEQUENCE FROM N.A.
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 RA WILSON J., AINSWORTH P., ANDERSON K., RAYNES C., PIPPS M., BRINLEY J.,
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 RA WILKINSON-SPROAT J., WOLDMAN P.
 FT * 2 3 ME 35 5 nucleotide sequence from chromosome 11 of C.
 RT elegans.
 RL NATURE 368:32-38(1994).
 DR EMBL: Z78415; E259012;
 SO SEQUENCE 925 AA; 99340 MW; C78CA124 CDS;

100.0% STISC 5 DB 31 Length 747 AA
 Best Local Similarity 100.0% Pred. No. 256-02
 Matches 51 Conservative 0 Mismatches 0 Indels 0 Gaps 0
 DB 555 STISC 559
 RESULT 5
 ID 093238 PRELIMINARY PRT 325 AA
 AC 093238
 DT 01-FEB-1997 (TREMURIEL 02, CREATED)
 DI 01-FEB-1997 (TREMURIEL 02, LAST SEQUENCE UPDATE)
 DE C17G1.4
 OS CAENORHABDITIS ELEGANS
 CC EUDARVOTA: METAZOA: NEMATODA: SEPERENTHEA: PHARODITIA: PHARODITIAE
 CC PHARODITIA: PHARODITIAE: PHARODITIAE: PHARODITIAE: PHARODITIAE: PHARODITIAE
 RN [1]
 RP SEQUENCE FROM N.A.
 RL WHITE S.
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 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 94150718
 RA WILSON J., AINSWORTH P., ANDERSON K., RAYNES C., PIPPS M., BRINLEY J.,
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 RA LEAF S., LEAF S., HERRIN P., HAVILL A., HUTTON J., JACOBIA A., JELLY P.,
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 RA WILKINSON-SPROAT J., WOLDMAN P.
 FT * 2 3 ME 35 5 nucleotide sequence from chromosome 11 of C.
 RT elegans.
 RL NATURE 368:32-38(1994).
 DR EMBL: Z78415; E259012;
 SO SEQUENCE 925 AA; 99340 MW; C78CA124 CDS;

Query Match	Score	DB 3:	Length	332:
Best Local Similarity	100.0%	Pred No. 1.2e+02		
Matches	5	Mismatches	0	Indels
			0	Gaps
			0	
QY	1	STSC	5	
	1	1	1	
	1	1	1	
db	230	STSC	234	

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DP      PFAM; PRO0065; neut_chan1_2; CHANNEL; GYROPHILIN; 1;KNNKNNKNNKNNK
NM      POSTSYNAPTIC MEMBRANE; JENNY;
SV      SEQUENCE 545 AA; 37201 MM; 2620775.00000;

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QY	1	STISC	5
Db	138	STISC	142

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RESULT      8
ID 047551      FTE:MINAPV:      PRT: 489 AA.
      047551:
AC 01-NOV-1996 (TREMBLREL_01, CREATED)
AD 01-NOV-1996 (TPERMREL_01, LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TREMBLREL_08, LAST ANNOTATION UPDATE)
DE PROLINE PERMEASE (FRAGMENT).
GN PUMP.
OS ESCHERICHIA COLI.
CC BACTERIA; PROTEOBACTERIA, GAMMA SUBDIVISION, ENTEROBACTERIAE;
OC ESCHERICHIA.
RN [1]
RF SEQUENCE FROM N.A.
RX MEDLINE: 93015751.
FA NELSON K.; SEANER R.K.;
BT "extracellular products of the proline permease gene (pump) and the
PI control region of the Escherichia coli ";
RT Salmonella and Escherichia coli ";
RL J. BACTERIOL. 174:6886-6895(1992).
DR EMBL: L01133; G147457;
DR PROSITE: PS00456; NA_SOLDI_STYLE_1;
DR PROSITE: PS00457; NA_SOLDI_STYLE_2;
DR PRAM: PR00474; SSF: 1.
FT NON-TER 489 489
SQ 489 AA: 52869 MW: 5803524E CPC32:

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Query Match      100.0%  Score 26; DB 9; Length 489;
Best Local Similarity 100.0%  Pident No. 1,8e+02;
Matches      5; Conservative      0; Mismatches      0; Indels      0; Gaps
                                1 STSC 5
                                |||||
DB      340 STSC 344

RESULT      9
047552
1L  047552      PRUIMINAEV      PPT      489 AA.
AC  047552;
U1  NOV-1996 (TEPMRIPEL_01 CREATED)
D1  01-NOV-1996 (TEPMRIPEL_01 LAST SEQUENCE UPDATE)
D1  01-NOV-1996 (TEPMRIPEL_08 LAST ANNOTATION UPDATE)
DE  PROLINE PEPMASE (PEPMASENT).
GN  PUMP.
OS  ESCHERICHIA COLI
OC  BACTERIA; FIRMICUTES; GAMMA SUPRIVISION; ENTEROBACTERIAE;
    ESCHERICHIA.
RN  [1]
RF  SEQUENCE FROM N.A.
RX  MEDLINE; 93015751.
FA  NELSON V., SFLANDEP P. K.;
RT  "Evolutionary genetics of the proline permease gene (putf) and the
    control region of the proline utilization operon in populations of
    Salmonella and Escherichia coli."
    J. BACTERIOL. 174:1987-1997(1992).
KL  EMER, EMITED. 5147443;
LN  PROSITE; PS00456; NA_S0LUT_SYM_1; 1.

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DE SITE 1504 71 NA_SOUT_SYP_2; 1.
 1. NAME: 171; SEQ: 1
 2. N NTER 489
 3. SEQUENCE 489 AA; 52804 MW; 2FA0A88 CRC32;

Query Match 100.0%; Score 26; DB 9; Length 489;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1. STISC 5
 2. STISC 5
 3. STISC 5

RESULT 11
 ID 054978 PRELIMINARY; PRT: 489 AA.
 AC 054978;
 DT 01-NOV-1996 (TREMBLREL, 01, CREATED)
 DI 01-NOV-1996 (TREMBLREL, 01, LAST SEQUENCE UPDATE)
 DR 01-NOV-1996 (TREMBLREL, 08, LAST ANNOTATION UPDATE)
 DE PROLINE PERMEASE (FRAGMENT)
 GN PUTP
 OS ESCHERICHIA COLI
 OC BACTERIA; PHOTOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
 ON ESCHERICHIA
 RN NELSON K. SELANDER R.K.;
 RX MEDLINE: 93015751.
 RA SEQUENCE FROM N.A.
 RT Evolutionary genetics of the proline permease gene (putp) and the control region of the proline utilization operon in populations of *Salmonella* and *Escherichia coli*.
 RI 1 BACTPP-VOL 174:689-6895(1992).
 RL EMBL: L01136; G154292;
 DR PROSITE: PS00456; NA_SOUT_SYP_1; 1.
 DR PROSITE: PS00457; NA_SOUT_SYP_2; 1.
 DR PFAM: PF00474; SSF: 1.
 FT NON_TER 489
 SO SEQUENCE 489 AA; 52804 MW; 197A0A06 CRC32;
 Query Match 100.0%; Score 26; DB 9; Length 489;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1. STISC 5
 2. STISC 5
 3. STISC 5

DR PROSITE: PS00456; NA_SOUT_SYP_1; 1.
 DR PROSITE: PS00457; NA_SOUT_SYP_2; 1.
 DR PFAM: PF00474; SSF: 1.
 FT NON_TER 489
 SO SEQUENCE 489 AA; 52804 MW; 7D1197RR CRC32;

Query Match 100.0%; Score 26; DB 9; Length 489;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1. STISC 5
 2. STISC 5
 3. STISC 5

RESULT 12
 ID 054978 PRELIMINARY; PRT: 489 AA.
 AC 054978;
 DT 01-NOV-1996 (TREMBLREL, 01, CREATED)
 DI 01-NOV-1996 (TREMBLREL, 01, LAST SEQUENCE UPDATE)
 DR 01-NOV-1996 (TREMBLREL, 08, LAST ANNOTATION UPDATE)
 DE PROLINE PERMEASE (FRAGMENT)
 GN PUTP
 OS SALMONELLA SP.
 OC BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
 ON SALMONELLA
 RN NELSON K. SELANDER R.K.;
 RX MEDLINE: 93015751.
 RA SEQUENCE FROM N.A.
 RT Evolutionary genetics of the proline permease gene (putp) and the control region of the proline utilization operon in populations of *Salmonella* and *Escherichia coli*.
 RI 1 BACTPP-VOL 174:689-6895(1992).
 RL EMBL: L01136; G154292;
 DR PROSITE: PS00456; NA_SOUT_SYP_1; 1.
 DR PROSITE: PS00457; NA_SOUT_SYP_2; 1.
 DR PFAM: PF00474; SSF: 1.
 FT NON_TER 489
 SO SEQUENCE 489 AA; 52804 MW; 4883A888 CRC32;

Query Match 100.0%; Score 26; DB 9; Length 489;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1. STISC 5
 2. STISC 5
 3. STISC 5

Db 340 STISC 344

RESULT 13
 ID 054979 PRELIMINARY; PRT: 489 AA.
 AC 054979;
 DT 01-NOV-1996 (TREMBLREL, 01, CREATED)
 DI 01-NOV-1996 (TREMBLREL, 01, LAST SEQUENCE UPDATE)
 DR 01-NOV-1996 (TREMBLREL, 08, LAST ANNOTATION UPDATE)
 DE PROLINE PERMEASE (FRAGMENT)
 GN PUTP
 OS SALMONELLA SP.
 OC BACTERIA; PROTEOBACTERIA; GAMMA SUBDIVISION; ENTEROBACTERIACEAE;
 ON SALMONELLA
 RN NELSON K. SELANDER R.K.;
 RX MEDLINE: 93015751.
 RA SEQUENCE FROM N.A.
 RT Evolutionary genetics of the proline permease gene (putp) and the control region of the proline utilization operon in populations of *Salmonella* and *Escherichia coli*.
 RI 1 BACTPP-VOL 174:689-6895(1992).
 RL EMBL: L01136; G154292;
 DR PROSITE: PS00456; NA_SOUT_SYP_1; 1.
 DR PROSITE: PS00457; NA_SOUT_SYP_2; 1.
 DR PFAM: PF00474; SSF: 1.
 FT NON_TER 489
 SO SEQUENCE 489 AA; 52804 MW; 4883A888 CRC32;

RL J. BACTERIOID 174:6886-6895(1992).
 DR EMBL: L01139: G154284.
 DR PROSITE: P80456: NA_SQUT_SYMP_1: 1.
 DR PROSITE: P80457: NA_SQUT_SYMP_2: 1.
 DR PIRAM: PF00474: SSF: 1.
 FT NON_TER 489 AA: 12367 MW: 641357.9 GP032.
 ST SEQUENCE 489 AA: 12367 MW: 641357.9 GP032.

Query Match 100.0%; Score 26; DB 9; Length 489;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STSC 5
 Db 340 STSC 344

RESULT 14
 ID 054980 PRELIMINARY: PRT: 489 AA
 AC 054980:
 DT 01-NOV-1996 (TREMELPEL_01, CREATED)
 DT 01-NOV-1996 (TREMELPEL_01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1996 (TREMELPEL_08, LAST ANNOTATION UPDATE)
 DE PROLINE PERMEASE (PPAGMENT).
 GN PUTP.
 OS SALMONELLA SP.
 OC BACTERIA: PROTEOBACTERIA: GAMMA SUBDIVISION: ENTEROBACTERIACEAE:
 OC SALMONELLA.
 RN 11
 RP SEQUENCE FROM N.A.
 RC STRAIN-S2983:
 RX MEDLINE: 93015751.
 PA NELSON K.; SELANDER R. K.;
 RI "Evolutionary genetics of the proline permease gene (putp) and the
 RI control region of the proline utilization operon in populations of
 RI *Salmonella* and *Escherichia coli*."
 RL J. BACTERIOID. 174:6886-6895(1992).
 DR EMBL: L01139: G154284.
 DR PROSITE: P80456: NA_SQUT_SYMP_1: 1.
 DR PROSITE: P80457: NA_SQUT_SYMP_2: 1.
 DR PIRAM: PF00474: SSF: 1.
 FT NON_TER 489 AA: 12367 MW: 641357.9 GP032.
 ST SEQUENCE 489 AA: 12367 MW: 641357.9 GP032.

Query Match 100.0%; Score 26; DB 9; Length 489;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STSC 5
 Db 340 STSC 344

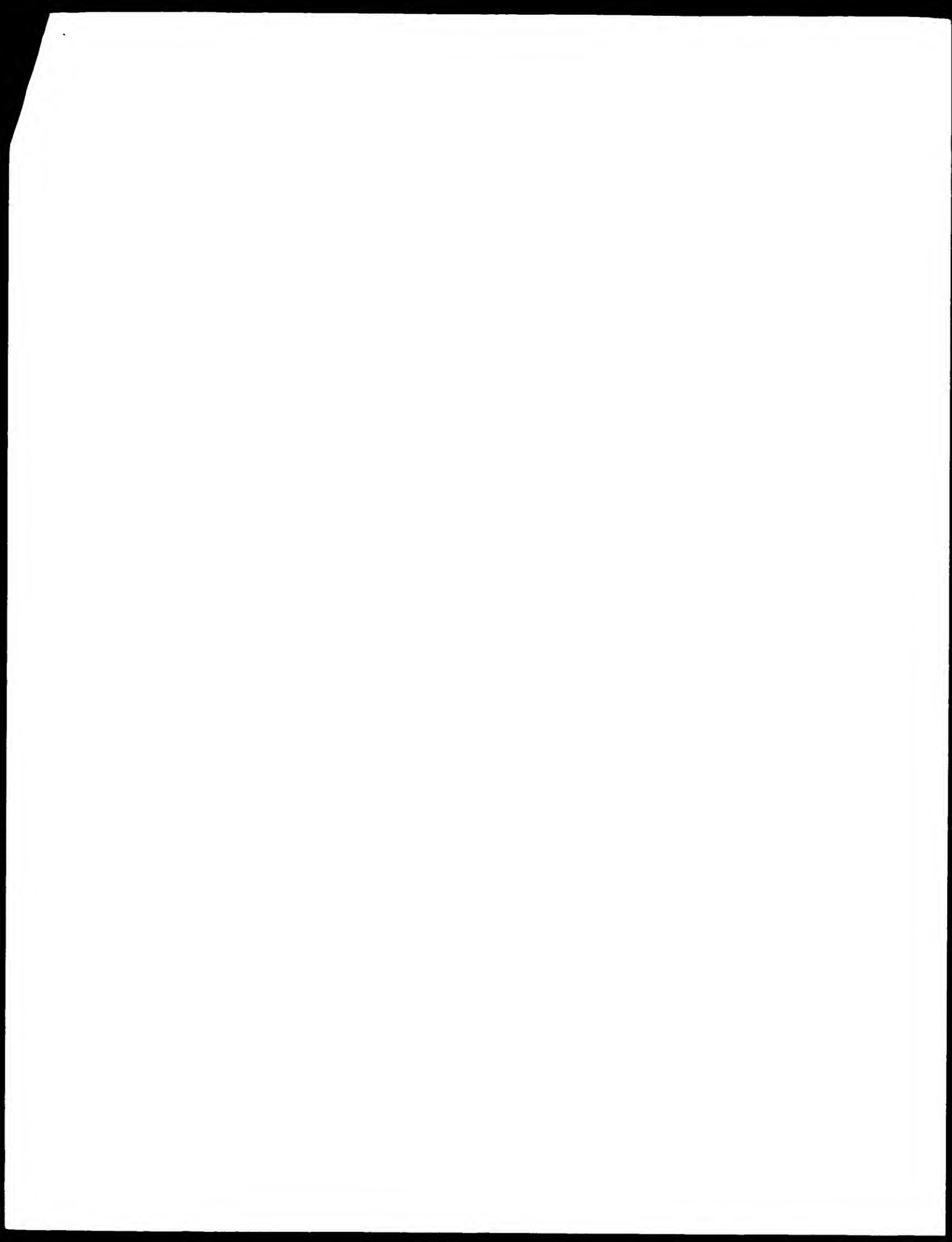
RESULT 15
 ID 054981 PRELIMINARY: PRT: 489 AA
 AC 054981:
 DT 01-NOV-1996 (TREMELPEL_01, CREATED)
 DT 01-NOV-1996 (TREMELPEL_01, LAST SEQUENCE UPDATE)
 DT 01-NOV-1996 (TREMELPEL_08, LAST ANNOTATION UPDATE)
 DE PROLINE PERMEASE (PPAGMENT).
 GN PUTP.
 OS SALMONELLA SP.
 OC BACTERIA: PROTEOBACTERIA: GAMMA SUBDIVISION: ENTEROBACTERIACEAE:
 OC SALMONELLA.
 RN 11
 RP SEQUENCE FROM N.A.
 RC STRAIN-S2983:
 RX MEDLINE: 93015751.
 RA NELSON K.; SELANDER R. K.;

RI "Evolutionary genetics of the proline permease gene (putp) and the
 RI control region of the proline utilization operon in populations of
 RI *Salmonella* and *Escherichia coli*."
 RL J. BACTERIOID. 174:6886-6895(1992).
 DR EMBL: L01139: G154284.
 DR PROSITE: P80456: NA_SQUT_SYMP_1: 1.
 DR PROSITE: P80457: NA_SQUT_SYMP_2: 1.
 DR PIRAM: PF00474: SSF: 1.
 FT NON_TER 489 AA: 12367 MW: 641357.9 GP032.
 ST SEQUENCE 489 AA: 12367 MW: 641357.9 GP032.

Query Match 100.0%; Score 26; DB 9; Length 489;
 Best Local Similarity 100.0%; Pred. No. 1.8e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 STSC 5
 Db 340 STSC 344

Search completed: June 22, 1999, 11:01:24
 Job time: 170 sec



025386 stimulus poi
025386 electrocortico

Run on: Tue 22, 1999, 10:59:45 ; Search time 45.16 Seconds

2.972 Million cell updates/sec

Title: US-03-0311-061-5

Sequence:

Scoring table: BIOSCM62

Searched: 74,19 seqs, 2684029 : 10/17/19

Database : SwissProt_36:4

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is used in the analysis of the total score distribution.

Result	Query	
No.	Score	Match length DB ID Description

1	26	100.0	320	1	AATP_PAT	P26617 ratius novae
2	26	100.0	789	1	ACOX_YEAST	P38551 saccharomyces
3	26	100.0	412	1	ECR2_BRAF	P08159 brachydanio
4	26	100.0		1	G156_PAPPE	P21857 parametium
5	26	100.0	2715	1	GAE2_RABU	P80339 tana rugosa
6	26	100.0	33	1	GAE2_RABU	P80339 tana rugosa
7	26	100.0	509	1	HYAL_HUMAN	P38557 homo sapiens
8	26	100.0	193	1	IL18_HUMAN	Q14116 homo sapiens
9	26	100.0	192	1	IL18_MOUSE	P70380 mus musculus
10	26	100.0	160	1	IL18_PIG	Q10073 sus scrofa
11	26	100.0		1	IL18_RAT	P27637 ratius norvi
12	26	100.0	830	1	LEP1_HUMAN	P16100 homo sapiens
13	26	100.0	984	1	MFR_HUMAN	P08231 homo sapiens
14	26	100.0	113	1	NAPF_HAFIN	P44650 haemophilus
15	26	100.0	720	1	NEA4_SCHPO	P41393 schistosoma
16	26	100.0	752	1	NEF2_DPOME	P54351 dioscorilla
17	26	100.0	502	1	PRTP_ECOLI	P07111 escherichia
18	26	100.0	502	1	PRTP_SALTY	P15502 salmonella
19	26	100.0		1	PRPH_CHTUY	P71714 chlamydia
20	26	100.0	406	1	PIR1_HCVVA	P16780 human cytome
21	26	100.0	177	1	VP22_ASEB7	P22160 artibeus
22	26	100.0	720	1	YX71_SCHPO	Q10320 schistosoma
23	26	100.0	840	1	YHT1_YEAST	P18835 saccharomyces
24	26	100.0	125	1	YVR3_YEAST	P29079 saccharomyces
25	26	100.0	125	1	YVR3_YEAST	P29079 saccharomyces
26	26	100.0		1	YVR3_YEAST	P29079 saccharomyces
27	26	100.0	819	1	CAE1_HAFIN	P45542 bacteroides
28	26	100.0	217	1	INF1_STEIT	P43820 haemophilus
29	26	100.0	1106	1	PDR1_HUMAN	P09614 human saphir
30	26	100.0	1008	1	PDR1_HUMAN	P09614 human saphir
31	26	100.0	652	1	PDR1_HUMAN	P09614 human saphir
32	26	100.0	97	1	PDR1_HUMAN	P09614 human saphir
33	26	100.0	125	1	YVR3_YEAST	P29079 saccharomyces
34	26	100.0	465	1	YVR3_YEAST	P29079 saccharomyces
35	26	100.0	1760	1	YVR3_YEAST	P29079 saccharomyces
36	26	100.0	1760	1	YVR3_YEAST	P29079 saccharomyces
37	26	100.0	1760	1	YVR3_YEAST	P29079 saccharomyces
38	26	100.0	1760	1	YVR3_YEAST	P29079 saccharomyces
39	26	100.0	1760	1	YVR3_YEAST	P29079 saccharomyces
40	26	100.0	1760	1	YVR3_YEAST	P29079 saccharomyces
41	26	100.0	1760	1	YVR3_YEAST	P29079 saccharomyces
42	26	100.0	1760	1	YVR3_YEAST	P29079 saccharomyces
43	26	100.0	1760	1	YVR3_YEAST	P29079 saccharomyces

	RESULT	1	ALIGNMENTS
AA3R_PAT	PAT	STANDARD	PET, 320 AA.
AC	P28647	0637922	(PEL_24, CREATED)
AD	WATER-1992	(PEL_24, LAST SEQUENCE UPDATE)	
DT	01-NOV-1997	(PEL_35, LAST SEQUENCE UPDATE)	
DE	15-JUL-1998	(PEL_36, LAST ANNOTATION UPDATE)	
GN	ADORA3		
OS	BACTUS NORVEGICUS (PAT),		
OC	EUBACTERIA, BETA-TA, DEBILATA, VERIEFATA, EUPHRODIA MAMMALIA,		
RP	SEQUENCE FROM N.A. AND TRANSCRIPTION.		
RC	TISSUE-BRAIN:		
RX	MEDLINE: 92366475		
RA	CHARD C S, HARRIS J, LAM M E, THOMSON P A, STILES J D, CYRILLI O J,		
PL	PROC NATL ACAD SCI U S A 89:7432-7436(1992).		
FN	[2]		
FP	SEQUENCE FROM N.A.		
PC	SPIRAL-MISTAY; TISSUE-TESTES;		
RX	MEDLINE: 91285122		
RA	MEYERHOFF W, MEYER-PRECHIN R, ROCHER D,		
EL	FEBS LETT. 294:155-160(1991).		
FN	[3]		
FP	SEQUENCE FROM N.A.		
RC	TISSUE-BRAIN:		
RX	MEDLINE: 96196578		
RA	SAUJANI F G, HOWE D I, DWANING P C, FIRESTEIN G S,		
EL	FEBS LETT. 382:125-129(1996).		
CC	- FUNCTION: RECEPTOR FOR ADENOSINE. THE ACTIVITY OF THIS RECEPTOR IS MODIFIED BY G PROTEINS WHICH INHIBITS ADENYLATE CYCLASE.		
CC	- POSSIBLE ROLE IN REPRODUCTION.		
CC	- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.		
CC	- TISSUE SPECIFICITY: TESTIS. PARTICULARLY IN SPERMATOGENES AND SPERMATIDS BUT NOT IN SPERMATOGENIA. LOW LEVELS IN THE BRAIN.		
CC	- DEVELOPMENTAL STAGE: EXPRESSED DURING SPERMIOGENESIS.		
CC	- ALTERNATIVE PRODUCTS: TWO FORMS ARE PRODUCED BY ALTERNATIVE SPLICING.		
CC	- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.		
DR	EMBL: X59249; G56308;		
DR	EMBL: M46153; G46032;		
DR	EMBL: X29215; Z219918;		
DR	FIR SI7777; S7777;		
DR	FIR, M46152; A6152;		
TF	GSTRB, GSE-0373;		
TF	GSTRB, GCR-0373;		
TF	GSTRB, GCR-1262;		
FA	HASHIGUCHI-SMOKETSU A, PROTEIN_RECEPTOR_1		
KK	G-PROTEIN-COUPLED RECEPTOR_TRANSMEMBRANE_CYTOPLASMIC		
KK	INTERPROTEIN: PALMITATE_ALTERNATIVE_SPLICING		
FT	DOMAIN 1	15	EXTRACELLULAR (POTENTIAL);
FT	TRANSXEM	39	1 (POTENTIAL);
FT	LCVAIT	10	CYTOPLASMIC (POTENTIAL);
FT	TRANSXEM	51	2 (POTENTIAL);
FT	DOMAIN	75	EXTRACELLULAR (POTENTIAL);
FT	TRANSXEM	106	3 (POTENTIAL);
FT	LCVAIT	139	CYTOPLASMIC (POTENTIAL);
FT	TRANSXEM	129	4 (POTENTIAL);
FT	LCVAIT	157	EXTRACELLULAR (POTENTIAL);
FT	TRANSXEM	189	5 (POTENTIAL);
FT	LCVAIT	201	CYTOPLASMIC (POTENTIAL);
FT	TRANSXEM	224	6 (POTENTIAL);
FT	LCVAIT	258	EXTRACELLULAR (POTENTIAL);
FT	TRANSXEM	284	7 (POTENTIAL);
FT	LCVAIT	297	CYTOPLASMIC (POTENTIAL);

CC CYSTEINES, EXCEPT FOR FOUR HALF PERIODS. A VARIABLE PART OF 475
 CC RESIDUES COMPRISES 4 ALMOST IDENTICAL PERIODS IN THE MIDDLE OF THE
 CC PROTEIN.
 CC -1- EXPRESSION OF 3 PROTEIN OCCURS AT LOW TEMPERATURES (14-32
 CC DEGREES CELSIUS).
 CC -1- SIMILARITY: 98% TO THE ALLELIC FORM 1686 PROTEIN (P17053) IN
 CC PERIODIC STRUCTURE AND 80% IN VARIABLE DOMAIN IN THE MIDDLE OF
 CC THE PROTEIN.
 DR EMBL: X03893; G578475; -
 DR PIR: A23475; A23475.
 DR HSPD: P06620; I1NA.
 KW SIGNAL: REPEAT: ANTIGEN: MEMBRANE: GPI-ANCHOR.
 FT SIGNAL: 1 20
 FT CHAIN: 21 275 1566 SURFACE PROTEIN
 FT DOMAIN: 106 2560 37 X 75 AA APPROXIMATE REPEATS.
 FT SPLIT: 1 222 89% TO PARALLEL: TETRAPEPTA A
 FT SEQUENCE: 275 AA; 27500 MW; GAFG5AA GPC32.

Query Match 100.0% Score 26; DB 1; Length 2715.
 Best Local Similarity 100.0% Pred. No. 3 Se-02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STISC 5
 DB 1487 STISC 1491

RESULT 5
 GAE2_RANRU STANDARD: PRI: 33 AA.
 AC P80396;
 DT 01-NOV-1994 (REL. 32, LAST SEQUENCE UPDATE)
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
 DE GAESURIN-2;
 OS RANA FUSCA (FROG);
 OC FRYAUYOTA METAZOA; CROCEATA. VERTEBRATA. TETRAPEPTA. AMPHIBIA. ANURA.
 RN [1]
 RP SEQUENCE.
 RC TISSUE=SKIN;
 RA MEDLINE: 95091844.
 RX PARK J.M., JUNG J.-E., LEE B.-J.;
 RL BIOCHEM. BIOPHYS. RES. COMMUN. 205:948-954(1994).
 CC -1- FUNCTION: HAS A NON-HEMOLYTIC ACTIVITY HAS A BROAD SPECTRUM OF
 CC ACTIVITY AGAINST BOTH GRAM POSITIVE AND GRAM NEGATIVE BACTERIA,
 CC FUNGI AND PROTOZOA.
 CC -1- SUBUNIT: MONOMER.
 CC -1- SUBCELLULAR LOCATION: SECRETED.
 CC -1- TISSUE SPECIFICITY: SKIN.
 CC -1- SIMILARITY: BELONGS THE PREVINCIN/ESULENIN/TACOPRIN/PUROSIN
 CC FAMILY.
 KW AMPHIBIAN SKIN. ANTIBIOTIC. BY SIMILARITY.
 FT DISULFID 27
 FT SEQUENCE 33 AA; 3322 MW; 96F2A97A GPC32.

Query Match 100.0% Score 26; DB 1; Length 33;
 Best Local Similarity 100.0% Pred. No. 7.3;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STISC 5
 DB 23 STISC 27

RESULT 6
 GAE2_RANRU STANDARD: PRI: 33 AA.
 AC P80397;
 DT 01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
 DT 01-NOV-1997 (REL. 32, LAST SEQUENCE UPDATE)

DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
 DE GAESURIN-3;
 OS RANA FUSCA (FROG);
 OC FRYAUYOTA METAZOA; CROCEATA. VERTEBRATA. TETRAPEPTA. AMPHIBIA. ANURA.
 RN [1]
 RP SEQUENCE.
 RC TISSUE=SKIN;
 RX MEDLINE: 95091844.
 RA PARK J.M., JUNG J.-E., LEE B.-J.;
 RL BIOCHEM. BIOPHYS. RES. COMMUN. 205:948-954(1994).
 CC -1- FUNCTION: HAS A NON-HEMOLYTIC ACTIVITY. HAS A BROAD SPECTRUM OF
 CC ACTIVITY AGAINST BOTH GRAM POSITIVE AND GRAM NEGATIVE BACTERIA,
 CC FUNGI AND PROTOZOA.
 CC -1- SUBUNIT: MONOMER.
 CC -1- SUBCELLULAR LOCATION: SECRETED.
 CC -1- TISSUE SPECIFICITY: SKIN.
 CC -1- SIMILARITY: BELONGS THE PREVINCIN/ESULENIN/TACOPRIN/PUROSIN
 CC FAMILY.
 KW AMPHIBIAN SKIN. ANTIBIOTIC. BY SIMILARITY.
 FT DISULFID 27
 FT SEQUENCE 33 AA; 3309 MW; A8160CB GPC32;

Query Match 100.0% Score 26; DB 1; Length 33;
 Best Local Similarity 100.0% Pred. No. 7.3;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STISC 5
 DB 23 STISC 27

RESULT 7
 HVAL_HUMAN STANDARD: PRI: 509 AA.
 AC P38567;
 DT 01-OCT-1994 (REL. 30, CREATED)
 DT 01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
 DT 15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
 DE HYALURONIDASE PRECURSOR (FC 3 2 1 35) (SPERM SUPPAP PROTEIN PG-20)
 GN SPAM OR HYAL OR H420.
 OS HOMO SAPIENS (HUMAN);
 OC FRYAUYOTA METAZOA; CROCEATA. VERTEBRATA. TETRAPEPTA. MAMMALIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=TESTIS;
 RX MEDLINE: 94052105.
 RA LIN Y., KIMMEL T.H., MYLES D.G., PRIMAROFF P.;
 RL FEBC NATL. ACAD. SCI. U.S.A. 90:10071-10075(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=TESTIS;
 RX MEDLINE: 94109604.
 RA GMAHL M., SAGAN S., KETTER S., KREIL G.;
 RL FEBS LETT. 336:545-548(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=TESTIS;
 RX MEDLINE: 96111393.
 RA JONES M.H., DAVEY P.M., APPLIN H., AFFARA N.A.;
 RL GENOMICS 29:196-800(1995).
 CC -1- FUNCTION: INVOLVED IN SPERM-EGG ADHESION. UPON FERTILIZATION
 CC SPERM MUST PENETRATE A LAYER OF CORIUS CELLS THAT
 CC SUPPORTS THE EGG BEFORE REACHING THE ZONA PELLUCIDA. THE
 CC CORIUS CELLS ARE EMBEDDED IN A MATRIX CONTAINING HYALURONIC
 CC ACID WHICH IS HYALURONIC ACID. THIS PROTEIN AIDS IN
 CC PENETRATING THE LAYER OF CORIUS CELLS BY DIGESTING HYALURONIC
 CC ACID.
 CC -1- CATALYTIC ACTIVITY: RANDOM HYDROLYSIS OF 1,4-LINKAGES BETWEEN
 CC N-ACETYL-GLUCOSAMINE AND D-GALACTOSAMINE RESIDUES IN
 CC HYALURONATE.

County Match	100.00%	Score: 26;	DB 1;	Length 193;
County Match	100.00%	Score: 34;		

	RESULT	10
IL18_PIG		
IL18_PIG	SI:ANAL:11	PR:1 190 AA
AC	019073;	
DT	15-JUL-1998 (REL, 36, CREATED)	
DT	15-JUL-1998 (REL, 36, LAST SEQUENCE UPDATE)	
DT	15-JUL-1998 (REL, 36, LAST ANNOTATION UPDATE)	
DE	INTERLEUKIN-18 PREPROPEP (IL 18) (INTERPEP-P-GAMMA INDUCING FACTOR)	
DE	(IFN-GAMMA-INDUCING FACTOR) (INTERLEUKIN-1 GAMMA) (IL-1 GAMMA)	
DE	(FRAGMENT).	
GN	IL18 OR IGIF.	
OS	SUS SCROFA (PIG).	
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TESTUDINATA; MAMMALIA;	
OC	EUARTHRA; ARTIODACTYLA.	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RA	FOSS D L, MORIADGH M.P.:	

Query Match: 100.0% Score 26; DB 1; Length 830;
 Best Local Similarity: 100.0%; Prod. No. 1.4e+02;
 Matches: 5; Conserved: 0; Mismatches: 0; Indels: 0; Gaps: 0;

11 STISC 5
 152 STISC 156

Query Match: 100.0% Score 26; DB 1; Length 830;
 Best Local Similarity: 100.0%; Prod. No. 1.4e+02;
 Matches: 5; Conserved: 0; Mismatches: 0; Indels: 0; Gaps: 0;

11 STISC 5
 152 STISC 156

Query Match: 100.0% Score 26; DB 1; Length 830;
 Best Local Similarity: 100.0%; Prod. No. 1.4e+02;
 Matches: 5; Conserved: 0; Mismatches: 0; Indels: 0; Gaps: 0;

11 STISC 5
 152 STISC 156

Query Match: 100.0% Score 26; DB 1; Length 830;
 Best Local Similarity: 100.0%; Prod. No. 1.4e+02;
 Matches: 5; Conserved: 0; Mismatches: 0; Indels: 0; Gaps: 0;

11 STISC 5
 152 STISC 156

Query Match: 100.0% Score 26; DB 1; Length 830;
 Best Local Similarity: 100.0%; Prod. No. 1.4e+02;
 Matches: 5; Conserved: 0; Mismatches: 0; Indels: 0; Gaps: 0;

11 STISC 5
 152 STISC 156

Query Match: 100.0% Score 26; DB 1; Length 830;
 Best Local Similarity: 100.0%; Prod. No. 1.4e+02;
 Matches: 5; Conserved: 0; Mismatches: 0; Indels: 0; Gaps: 0;

11 STISC 5
 152 STISC 156

Query Match: 100.0% Score 26; DB 1; Length 830;
 Best Local Similarity: 100.0%; Prod. No. 1.4e+02;
 Matches: 5; Conserved: 0; Mismatches: 0; Indels: 0; Gaps: 0;

11 STISC 5
 152 STISC 156

Query Match: 100.0% Score 26; DB 1; Length 830;
 Best Local Similarity: 100.0%; Prod. No. 1.4e+02;
 Matches: 5; Conserved: 0; Mismatches: 0; Indels: 0; Gaps: 0;

11 STISC 5
 152 STISC 156

Query Match: 100.0%; Score 26; DB 1; Length 113;
 Best Local Similarity: 100.0%; Pred. No. 21;
 Matches: 5; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 1 STRSC 5
 DB 17 STRSC 21

RESULT 13
 ND4_SCHPO STANDARD: PRT: 720 AA.
 ID ND4_SCHPO
 AC P41389;
 DT 01-NOV-1995 (REL. 32, CREATED)
 DI 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
 DI 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE CELL DIVISION CONTROL PROTEIN ND4.
 GN ND4 OR SPAC3F10.01.
 OS SCHISTOSOMULUS POMBE (FISSION YEAST).
 OC EUKARYOTA; FUNGI; ASCOMYCOTINA; HEMIASCOCYCETES.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 94129084.
 RA MIYAKE S, KISHITA N, SAWATAMA I, HIRAKAWA Y, IOTA T, SAITOH I,
 RA YANACIDA M;
 RL MOL. BIOL. CELL 4:1003-1015(1993).
 RN [2]
 RP SEQUENCE OF 72-720 FROM N.A.
 RC STRAIN=9712;
 RA MURPHY I, HARRIS D, BARRETT R.G., PALANDREAN M.A., WALSH S.V.;
 RL SUBMITTED (FEB-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
 CC - FUNCTION: ROLE IN DNA REPLICATION AND ESSENTIAL FOR VIABILITY.
 CC - STRUCTURAL LOCATION: NUCLEAR (POTENTIAL).
 CC - SIMILARITY: BELONGS TO THE MCM FAMILY.
 DR EMBL: 568467; G545211; -;
 DR EMBL: 569260; E211200; -;
 DR PIR: A48723; A48723;
 DR PROSITE: PS20847; MCM_1; 1;
 DR PROSITE: PS20851; MCM_2; 1;
 KW TRANSCRIPTION REPLICATION; DNA-BINDING; NUCLEAR PROTEIN;
 KW DNA REPLICATION; CELL CYCLE; ATP-BINDING;
 FT DOMAIN 307 312 POLY-GLU.
 FT DOMAIN 322 329 MCM.
 FT NP_BIND 372 379 ATP (POTENTIAL).
 FT CONFLICT 461 461 A -> R (IN REF. 1).
 SO SEQUENCE 720 AA; 90099 MW; 22261458 CDS32;

Query Match: 100.0%; Score 26; DB 1; Length 720;
 Best Local Similarity: 100.0%; Pred. No. 1,1e+02;
 Matches: 1; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

QY 1 STRSC 5
 DB 154 STRSC 158

Search completed: June 22, 1999, 10:59:46
 Job time: 72 sec



$\frac{1}{2} \left(\frac{1}{2} + \frac{1}{2} \right) = \frac{1}{2}$

McL. 1147098. *Parasitica*, 59: 27-32, 1989
A title, cloning and analysis of the gene encoding the 270 kDa cell surface
C. Accession: AF5532, AF5531
R. Lewis, A.P.
Mol. Biochem. Parasitol., 59: 27-32, 1989

```

C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1993 #sequence_revision 02-Jun-1994 #next_update 14-Sep-1994
C:Accession: S15661, S19108
R:Rutheford, M.N.; Kumar, A.; Nissim, A.; Chebath, J.; Williams, P.R.;
Nucleic Acids Res. 19, 1917-1924, 1991
A:Title: The murine 2.5A synthase locus
A:Reference number: S15661, MIM:6123062
A:Accession: S15661
A:Molecule type: mRNA
A:Residues: 1192-1925
A:Cross references: EMBL:X55982
R:Williams, B.
submitted to the EMBL Data Library, September 1990
A:Reference number: S19108
A:Accession: S19108
A:Molecule type: mRNA
A:Residues: 1175-1177, 177-192<MIL>
A:Cross references: EMBL:X55982; NID:q49714; PID:q49715
C:Specificity: 2110(A) synthase
C:Keywords: nucleotidyltransferase

Query Match          9.3%  Score 75.5  DB 2  Length 162
Best Local Similarity 23.2%  Pred. No. 2.6
Mismatches 50  Indels 48  Gaps 42

07  55  SLEHKAATISVCEKILSLSPKTSFKRNPEKILKSLI  ----- 103
      ||| ||| ||| ||| ||| ||| ||| ||| |||
28  57  -----NVFPHSLSPSPALSPKLSAPQLKELVILVAYELHLMK 104
      ||| ||| ||| ||| ||| ||| ||| ||| |||
09  101  -----FQPR---SP-CHQKMKFESSSEYEFACI---KEDLKI-----KEDDEL 147
      ||| ||| ||| ||| ||| ||| ||| ||| |||
10  104  PNFQFANLISVPAKREKILSEFWLQKHLN-PRKLPKLP-PRVAVYDLEKID 161
      ||| ||| ||| ||| ||| ||| ||| ||| |||
07  146 D 146
      |
10  143 D 143

RESULT 11
146620
Sus scrofa protointerleukin-1 alpha mRNA, complete cds - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #next_update 04-May-1997
C:Accession: 146620
R:Maliszewski, G.
Nucleic Acids Res. 14, 4282, 1990
A:Title: Nucleotide sequence of porcine interleukin-1 alpha
A:Reference number: 146620
A:Accession: 146620
A>Status: preliminary, translated from GR/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-270<MAL>
A:Cross references: GR:M8773; NID:q44622; PID:q44622
C:Specificity: interleukin-1

Query Match          9.3%  Score 75.5  DB 2  Length 270
Best Local Similarity 20.6%  Pred. No. 3.8
Mismatches 59  Indels 11  Gaps 50

07  6  KLSVLENNQVFLQYNNRPHRM-----SQCPRNAPETFLISYKSGYGRNAV 62
      ||| ||| ||| ||| ||| ||| ||| ||| |||
12  12  KYSKAVLNLTNNAFNLLIFSSLYMAAVLNLEAVLMAALIDNQLPV 184
      ||| ||| ||| ||| ||| ||| ||| ||| |||
07  62  TISVCKEKLSTSCENKLTSEKEM NPDNLRKRSGLIPQGVSVNHNKNGSSSY 12
      ||| ||| ||| ||| ||| ||| ||| ||| |||
10  184  TIRISIRFVSQNPDPAVILKEIPETPKTILEFTMK-----DQNMVKKSAH 244

```

Q: 121 ESTABLISHED 121
Db 230 PRT:ATPOTF 243

RESULT 12

A:serine/threonine-specific protein kinase cot, 52k form - human
A:Accession: A48713
N:Alternate names: cot proto-oncogene, 58k form
N:Contains: serine/threonine-specific protein kinase cot, 52k form
C:Species: Homo sapiens (Man)
C:Date: 07-Apr-1994 #sequence-revision 18-Nov-1994 #text-change 10-Jul-1998
C:Accession: A48713; B48713; S31639
J:Atoki, M.; Hamada, F.; Sugimoto, T.; Sumida, S.; Akiyama, T.; Toyoshima, K.
J:Biochem J 269: 2273-2279, 1993
A:Title: The human cot proto-oncogene encodes two protein serine/threonine kinases with
A:Reference number: A48713; M01D:3404034
A:Accession: A48713

A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-457
A:Experimental source: TCO-4 cells
A:Note: Sequence homologous with p34^{cdc2} transfection
A:Note: Sequence extracted from NCI backbone (NCBI:138970, NCBI:138972)
A:Accession: B48713
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 30-457 <A02>
A:Experimental source: TCO-4 cells
A:Note: sequence inconsistent with nucleotide translation
A:Note: sequence extracted from NCI backbone (NCBI:138970, NCBI:138972)
A:Accession: B48713; M: Aarssen, S.A.; Miki, T.; McGovern, E.S.
A:Title: A M. Chodis, M. Aarssen, S.A.; Miki, T.; McGovern, E.S.
A:Description: A transforming gene isolated by expression cloning from Ewing's sarcoma
A:Reference number: S31639
A:Accession: S31639
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-457
A:Cross-references: EMBL:14139, NID:931244; PID:931245
C:Superfamily: protein kinase homology
C:Keywords: alternative initiator; proto-oncogene
F:138-389/Lowdell; protein kinase homology <KIN>

Query Match 9.3% Score 75.5; DB 2; Length 467;
Best Local Similarity 22.1%; Pred. No. 7.4;
Matches 31; Conservative 25; Mismatches 39; Indels 45; Gaps 7;

Q: 13 FRNAGVFFFGNFFFEFTSTG.....DNAPFTF-----ISMV 52
Db 333 RSNVSYIYIHKQAPLEAD-DQSPGRELLEASLERPNRPRAADLKHEALNP 391
Q: 53 KDSQPPAAVITVKCEITSLSENK-IISFKENPNPNKDT-----KSLITFOR 104
Db 302 FETDPP.....QSLDSALIEPKPLSPKLELPENLADSSGTSSEEMLROR 442
Q: 105 SVPRCHNMGFESSYEYF 124
Db 443 S-----LYIDLGLALGYF 455

RESULT 13

ret protein - chicken
C:Species: Gallus gallus (chicken)
C:Date: 10-Oct-1995 #sequence-revision 03-Nov-1995 #text-change 19-Dec-1997
C:Accession: S57450
R:Robertson, K.; Mason, J.
Suk, T.; et al. FMP 374 Library June 1995
A:Description: Extracted from chicken embryo suggests roles in regionalisation
A:Reference number: S57450
A:Accession: S57450

A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1064
A:Cross-references: EMBL 24499, NID 987041, FID 987042
C:Superfamily: protein-tyrosine kinase ret; protein kinase homology
C:Keywords: ATP
F:714-1004/Domain; protein kinase homology <KIN>
F:722-730/Region; protein kinase A1 binding motif

Query Match 9.2% Score 75; DB 2; Length 1064;
Best Local Similarity 22.4%; Pred. No. 22;
Matches 38; Conservative 29; Mismatches 56; Indels 48; Gaps 7;

Q: 15 LNRGVFFGSKNPLFEFTSTG.....DNAPFTF-----ISMV 52
Db 107 LSNVSYIYIHKQAPLEAD-DQSPGRELLEASLERPNRPRAADLKHEALNP 391
Q: 75 SKENKTSFKNPNPNITKSDIFFPQSVPHDNKCESSYEYFAGE----- 129
Db 152 SKENKTSFKNPNPNITKSDIFFPQSVPHDNKCESSYEYFAGE----- 129
Q: 129 SKENKTSFKNPNPNITKSDIFFPQSVPHDNKCESSYEYFAGE----- 129
Db 206 NENIGVSVTQRIPEPEPEYELLAKQIVAGGFPEMEVEPELVNDED 255

RESULT 14

proto-oncogene protein - mouse
A:Accession: 149609
C:Date: 02-Jul-1994 #sequence-revision 02-Jul-1996 #text-change 10-Jul-1998
C:Accession: 149609
R:Ohata, R.; Miyoshi, J.; Aoki, M.; Toyoshima, K.
Jpn J Cancer Res 84: 518-525, 1993
A:Title: The murine cot proto-oncogene: genome structure and tissue-specific expression
A:Reference number: 149609; M01D:93308016
A:Accession: 149609
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-467
A:Cross-references: GDB:93309; NID:9296072; PID:9296073
C:Genetics: cot
A:Gene: cot
C:Superfamily: protein kinase homology
F:722-730/Domain; protein kinase homology <KIN>

Query Match 9.2% Score 75; DB 2; Length 467;
Best Local Similarity 21.0%; Pred. No. 8.2;
Matches 29; Conservative 22; Mismatches 36; Indels 34; Gaps 6;

Q: 12 FRNAGVFFFGNFFFEFTSTG.....DNAPFTF-----ISMV 52
Db 361 MPETFAAFENPNPFAVNLKHEALNPF-----EDGFE-----QSL 401
Q: 72 SLSTENK-IISFKENPNPNKDT-----KSLITFOR 104
Db 402 TSAIPFPPLSKRIQFPVAVSSGTSSEEMLROR 442
Q: 124 F 124
Db 455 F 455

RESULT 15

H64245
hypothetical protein MG414 - Mycoplasma genitalium (MG414)
C:Species: Mycoplasma genitalium
C:Date: 10-Nov-1994 #sequence-revision 10-Nov-1995 #text-change 13-Sep-1998
C:Accession: H64245
R:Fraser, C.M.; Gooyang, J.D.; White, O.; Adams, M.D.; Clayton, P.A.; Fleischmann, R.
M.; Finkman, D.; Nguyen, D.; O'Brien, A.D.; Saitoh, T.M.; Phillips, G.A.; Weirick,

[illegible]

[illegible]

```

RESULT 12
Y414_MYGE ID Y414_MYGE STANDARD: PRF: 1036 AA.
P47653;
D1 01-FEB-1996 (REL. 33, CREATED)
D1 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
L1 01-NOV-1997 (REL. 45, LAST ANN-OTATION UPDATE)
DE HYPOTHETICAL PROTEIN MG414.
CN MG414.
OS MYOPLASMA GENITALIUM.
OC PEROXYASA. TENDITUTIS. MOLLITUBS. MYOGLASMA. M. LANSATAEST.
OC MYOPLASMATAGEAE.
[1]
PP SEQUENCE FROM N.A.
RC STAIR-A.TC 35530 / G-37;
RX MEDLINE: 96026346.
RA FRASER G.M., GOCCANE J.D., WHITE O., ADAMS M.D., CLAYTON R.A.,
RA FLEISCHMAN R.D., RITT G.I., KERRAVAN A.P., SUTTON G., KELLEY J.M.,
RA EICHSMAN J.L., WEIDMAN J.F., SMALL R.V., SANDREY B., FERMAN J.J.,
RA NGREN D.T., HINTERHA T.R., SAUER D.M., PHILLIPS G.A., MEIERICK J.M.,
RA TOWR J.-F., DOUGHERTY R.A., BOETT K.F., HU P.-G., HODDER I.S.,
RA PETERSON S.N., SMITH H.O., HUTCHISON G.A., III, VENTRE L.O.,
RA SCIENCE 270:397-403(1995).
[2]
RN SEQUENCE OF 52-146 FROM N.A.
RC STRAIN-ATCC 35530 / G-37;
RX MEDLINE: 94075230.
RA PETERSON S.N., HU P.-G., BOETT K.F., HUTCHISON G.A., III,
RL J. BACTERIOLOGY 175:7918-7930(1993).
[3]
DE SMILASTY EPITOMES FOR THE MG414 / MG414 FORMIC.
DR EMEL: 030723; G1046129; -
DR EMEL: 001625; G405988; -
DR TIGR: MG414; -
DR HYPOHETICAL PROTEIN: TRANSEMBRANE.
RW TRANSMEM 4 24 POTENTIAL.
T1 TRANSMEM 1004 1024 POTENTIAL.
D2 SEQUENCE 1036 AA; 103176 MW; 7026445 SP032;
Query Match 4.1% Score 74.5; DB 1; length 1036;
Best Local Similarity 21 aa; Prod No 20;
Matches 33; Conservative 32; Mismatches 65; Indels 21; Gaps
14
NUNNMVFTHQGRREFPEE-MISECEFNAPHILFLISMWNSQGRAMVLSSAGGG 71
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
94* SNNGKLVLRNTHTTFSTCTTRVVAFNFNPFTFIHLVENVDFNRNTFRVWRF 964
71 -ISTSGSTIIISKENMFENIKTKSKELLIPGVSVSHNNMGALSSVYVNDIAADR 129

```


GenCode version 4.5
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OM proteins : protein search using sw model

Run on: 1999-11-01 14:24, Search time 83.17 seconds

(without alignments)
104 143 Million cell updates/sec

File: US-09-030-061-6

Sequence: 1 YVCKLESLVSNINPQVL..... LKREDELQDSIMTVQNEED 157

Scoring table: P1-Score2

Searched: 180763 seqs, 55169189 residues

Database:

SPTREML-8:
1: SP_fungi:
2: SP_human:
3: SP_invertebrate:
4: SP_mammal:
5: SP_mnc:
6: SP_oranella:
7: SP-phage:
8: SP-plant:
9: SP_bacteria:
10: SP_ricketia:
11: SP_virus:
12: SP_vertebrate:
13: SP_unclassified:
14: SP_archaea:

Pred No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution

SUMMARIES

Result No.	Score	Query Match	Length	TP	TF	Description
1	806	98.0	193	2	075599	075599 homo sapien
2	775	97.2	194	19	088749	088749 rattus norv
3	80.5	11.0	270	1	043031	043031 schizosacch
4	81.5	10.4	381	1	043031	043031 schizosacch
5	81.5	10.0	617	3	025986	025986 plasmodium
6	80.5	9.5	866	3	044500	044500 chlamydia t
7	80.5	9.5	4470	12	040041	040041 gallus gall
8	79	8.4	452	6	088821	088821 mus musculi
9	78	9.6	473	3	016673	016673 caenorhabdi
10	77.5	9.5	270	4	028985	028985 caenorhabdi
11	77.5	9.5	1251	12	091365	091365 coturnix co
12	76.5	9.4	425	3	030390	030390 caenorhabdi
13	76	9.3	632	8	080569	080569 arabidopsis
14	75	9.3	747	8	088293	088293 arabidopsis
15	75.5	9.3	457	2	014275	014275 homo sapien
16	75.5	9.3	270	4	077077	077077 plasmodium
17	75.5	9.3	192	10	060856	060856 mus musculi
18	75	9.2	1183	3	018080	018080 caenorhabdi
19	75	9.2	445	12	057510	057510 scyllarhin
20	75	9.2	1054	12	040041	040041 gallus gall
21	74.5	9.1	1970	2	023699	023699 caenorhabdi
22	74.5	9.1	137	3	077077	077077 plasmodium
23	74.5	9.1	351	3	083050	083050 liponema p
24	74	9.1	270	4	046613	046613 felis silve
25	74	9.1	10	070458	070458 mus musculi	
26	74	9.1	407	10	063552	063552 rattus norv
27	74	9.1	970	10	088821	088821 mus musculi
28	74.5	9.0	475	3	016673	016673 caenorhabdi
29	74.5	9.0	905	4	024954	024954 mycoplasma

ALIGNMENTS

30	73.5	9.0	389	14	010031	010031	attenuata
31	72.2	8.9	4590	12	014517	014517	homo sapien
32	72.2	8.9	447	3	018179	018179	caenorhabdi
33	72.1	8.8	586	3	045898	045898	caellius so
34	71.7	8.5	1	1	044517	044517	homo gallu
35	72.2	8.8	1792	12	040041	040041	gallus gall
36	71.5	8.8	1245	1	012276	012276	saccharomy
37	71.1	8.8	123	1	024214	024214	caenorhab
38	71.5	8.8	268	4	079161	079161	capra hirc
39	71.1	8.7	1921	3	024755	024755	caenorhab
40	71.1	8.7	1367	3	077354	077354	plasmodium
41	70.5	8.6	753	3	017590	017590	caenorhabdi
42	70.4	8.4	1278	3	044907	044907	perilla bu
43	70.4	8.6	659	3	044902	044902	saccharab
44	70.0	8.5	1739	3	076329	076329	dictyostel
45	70.0	8.4	1493	3	077319	077319	plasmodium

ALIGNMENTS

RESULT	1	
075599	PRELIMINARY:	PRT: 193 AA.
ID	075599	
AC	075599:	
DI	01-NOV-1998 (TREMBLREL, 08, CREATED)	
DT	01-NOV-1998 (TREMBLREL, 08, LAST SEQUENCE UPDATE)	
DE	01-NOV-1998 (TREMBLREL, 08, LAST ANNOTATION UPDATE)	
DE	INTERLEUKIN-18 PRECURSOR.	
IL18.		
OS	HOMO SAPIENS (HUMAN).	
OC	EUCHARYOTA: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA:	
OT	PRIMATES: CATARRHINI: HOMINIDAE: HOMO.	
OT	[1]	
RP	SEQUENCE FROM N.A.	
PA	YONG D., GUJIN D., LIHA H., HAITAO W.:	
FI	"Cloning and sequencing of the cDNA for precursor hIL-18."	
FI	Submitted (Jul-1998) to EMBL/GenBank/DDBJ Data Banks.	
DR	EMBL: AF077611; G348071; -	
KW	SIGNAL.	
FT	SIGNAL	1 36 POTENTIAL.
FT	CHAIN	37 193 INTERLEUKIN-18.
SI	SEQUENCE	193 AA; 22033 KM; 8100223 CDS22;

Query Match	98.0%	Score 850, DB 27	Length 193:
Best Local Similarity	98.1%	Prod No 170-63:	
Matches 154:	Conservative	1: 154 matches	2: 100cils
		0: Gaps	0

07	1	VFSLSEKLVANR NNVVFTFQVQHPPEVVLSTFQNGGPTFTTQNGKSTFQNG	30
08			
09	17	VFSLSEKLVINRNMGVFTFQVQHPPEVVLSTFQNGGPTFTTQNGKSTFQNG	35
10			
11	51	AVTTSVETSTSTSTPTSTFQNGGPTFTTQNGKSTFQNGGPTFTTQNGKSTFQNG	120
12			
13	97	AVTTSVQENST	154
14			
15	171	FOFTLAKETFT	157
16			
17	157	FOFTLAKETFT	193
18			

RESULT 2

075599	PRELIMINARY:	PRT: 194 AA.
ID	088749	
AC	088749:	
DI	01-NOV-1998 (TREMBLREL, 08, CREATED)	
DT	01-NOV-1998 (TREMBLREL, 08, LAST SEQUENCE UPDATE)	
DE	01-NOV-1998 (TREMBLREL, 08, LAST ANNOTATION UPDATE)	
DE	INTERLEUKIN-18.	
IL-18.		
OS	RATTUS NORVEGICUS (RAT).	
OC	EUMETAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA:	

DB 287 --LKMEALKEGJVLDPDYVBNENKKTMLLD 320

RESULT 6
ID 084500 PRELIMINARY: PRI: 866 AA.
AC 084500:
DI 01-NOV-1998 (TREMPEL, 02, CREATED)
DI 01-NOV-1998 (TREMPEL, 02, LAST SEQUENCE UPDATE)
DI 01-NOV-1998 (TREMPEL, 08, LAST ANNOTATION UPDATE)
DE DNA PRIMERASE 1
GN POLA.
OS CHLAMYDIA TRACHOMATIS.
OC BACTERIA: CHLAMYDIALES: CHLAMYDIACEAE: CHLAMYDIA.
RN
RP SEQUENCE FROM N.A.
RC STEPHENS P S, KALMAN S, LAMMEL C J, FAN J, MAPATHE P, ARAVIND L,
RA MITCHELL W P, OLINGER L, TATISOV P L, ZHAO Q, KOONIN E V,
RA DAVIS R W:
PT "Genomic Sequence of an Obligate Intracellular Pathogen of Humans:
PT Chlamydia trachomatis".
RC SCIENCE 0:0-0(1998).
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN=JW-3/EX;
RA STEPHENS P S, KALMAN S, LAMMEL C J, FAN J, MAPATHE P, ARAVIND L,
RA MITCHELL W P, OLINGER L, TATISOV P L, ZHAO Q, KOONIN E V,
RA DAVIS R W:
FL SPERMATITIS (MAY 1998); 11 EMP; 8,646,619; DATA BANKS.
DR EMBL: AEO01223; G3329229; -
SQ SHORFNC 866 AA; 96583 MW; 5088000A CRC32;

Query Match 6 98: Score 80 5; DB 9; Length 866;
Best Local Similarity 26.4%; Pred. No. 23;
Matches 45; Conservative 29; Mismatches 29; Indels 45; Gaps 9
CY 1 YKATKTKSVTRNNGVFF...TQGNRETFEEMT...-----STGDNATHTTII 49
DB 441 YKMLAKKIKAIK...YTFVLEEKELKCFEIVHQH EAVLFAWER-----V 496
CY 50 SMVQKTFEFAV...TTSYCKEKIS...TSCENKTSFEKEMN-----V 91
DB 447 QWETSS--GAVTFRTTTELEESGELVYLWCGENMISFGLSTIIYVQGIETPER 444
CY 92 TKTAKST 100
DB 545 AKSKAKAVL 553
RESULT 7
ID 090681 PRELIMINARY: PRI: 2470 AA.
AC 090681:
DI 01-NOV-1998 (TREMPEL, 01, CREATED)
DI 01-NOV-1998 (TREMPEL, 01, LAST SEQUENCE UPDATE)
DI 01-NOV-1998 (TREMPEL, 08, LAST ANNOTATION UPDATE)
DE CATION-DEPENDENT MANNOSE-6-PHOSPHATE RECEPTOR
OS GALLUS GALLUS (CHICKEN).
OC FRATRYIA VETATA: FRATRYIA VERTEBRATA: ANCHOROPRIA AVES.
OC NEOGNATHAE: GALLIFORMES: PHASIANIDAE: PHASIANINAE: GALLUS.
RN
RP SEQUENCE FROM N.A.
RC MEDLINE 2600469;
RA ZHOU M, MA Z, SU W S:
PT "Cloning and expression of the cDNA of chicken cation-independent
PT mannose-6-phosphate receptor".
PI PROC NATL ACAD SCI U S A 92 9762-9766(1995).
DR EMBL: U35037; G1019119; -
DR PFAM: PF00040; fn2; 1
DR PFAM: PF00579; CTR_repeat; 13
DR PFAM: PF00579; CTR_repeat; 13
SQ SEGNHCH 2170 AA; 27645 MW; 4086676 CRC32;

Query Match 9.84: Score 80; DB 12; Length 2470;
Best Local Similarity 25.9%; Pred. No. 90;
Matches 45; Conservative 30; Mismatches 51; Indels 18; Gaps 12;
CY 4 KIESLSTPNINPND---GVLETFQGNPFIFETMTISQSPNAPRI--VF GSNV----- 54
DB 1457 KIESPELMAIE--EYSLFWTAACPL-RSNV--NDQVNNVNAI3HLEFLISAKESQY 1515
CY 54 ---TSPP-----GMAVTI-----SVKPEYR--HSPN--H--LKEM 86
DB 1516 TITSHNKPFIINVAKASSQANSAVAVHIDPKTLNALSLLILYKLVKLVK 1575
CY 87 ND-PNINKT-KSOTIFPQSVPOHNRK---MPESSSYRYP-----LAPKE 130
DB 1576 TQPHHAKHPSYSEVQKASLSS-PVLSDEK--DQVYSWMLAELLE 1529

RESULT 8
ID 025249 PRELIMINARY: PRI: 452 AA.
AC 025249:
DI 01-JAN-1998 (TREMPEL, 05, CREATED)
DI 01-JAN-1998 (TREMPEL, 05, LAST SEQUENCE UPDATE)
DI 01-NOV-1998 (TREMPEL, 08, LAST ANNOTATION UPDATE)
DE HYPOTHETICAL 52.7 KD PROTEIN.
GN HPO508.
OS HETEROCHLIER PYDORI (CAMPYLOBACTER PYDORI).
OC BACTERIA: B--FEROCHLIERIA: FIETION SREVISOR: FEROCHLIERIA: B--FEROCHLIERIA.
OC HELICOBACTER.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=26695;
RC MEDLINE: 97394467;
RA TOMB J F, WHITE C, KERVAVAGE A P, CLAYTON R A, SUTTON G G,
RA FITZGERALD P D, KETCHUM F A, KLEIN R E, JILL S, ROBERTS B A,
RA NELSON K, QUACKENBUSH J, ZHOU L, KIRKNESS F F, PETERSON S,
RA NELSON K, FITZGERALD L M, LEE N, ADAMS M D, HICKY E K,
RA HOPKIN E, GAYNE J D, WILHELM L, FLEISCH J F, PETER J M,
RA COTTON M D, WEIDMAN J M, FUJII G, ROMAN G, WATNEY L, WALLIN E,
RA HAYES W S, ROBERTS M, KAP P D, SMITH H O, HANSEN J M,
RA VENTER J C:
PT "The 52.7 kDa sequence of the 52.7 kDa H. pylori
PT protein (published extratum appears in Nature 1997 Sep
PT 375(6549):412)."
RI 25,289(6549):412;
RL NATURE 388:539-547(1997).
DR EMBL: AEO00565; G2213624; -
DR TIGR: HPO508; -
KM HYPOTHETICAL PROTEIN.
SQ SEGNHCH 452 AA; 5,085 MW; 7619020 CRC32;

Query Match 9.74: Score 79; DB 9; Length 452;
Best Local Similarity 24.8%; Pred. No. 14;
Matches 45; Conservative 3; Mismatches 29; Indels 18; Gaps 12;
CY 4 GAVINLNNVETITJPHLEECMTSTRLNMFHHSKHSCTF----- 59
DB 146 TAVVWNNNA HIAHGELEYLFAVINININISLLVILNDLKAANLAVAN 103
CY 59 -GMAVTSVKCEKISLSCEN-KIISFEKPNPINDIKSDIIFQFVGHQ-----NK 112
DB 154 TVAVTVITNTINILSEIELELHEL-----TSVTKSTFTEF-VDQVAGTQX 219
CY 119 MFESSSYEDF---LACEKQLFLLEKKEDELSKSLMTVUN- 156
DB 220 TATSSKNNVAVYINVVFHFFVIVFIFERHRTISGHEHLEFL 166
RESULT 9
ID 016673

10 33 PRELIMINARY: PRI: 473 AA.
 11 33
 12 33 (PRELIMINARY: 05, CREATED)
 13 33 (PRELIMINARY: 05, LAST SEQUENCE UPDATE)
 14 33 (PRELIMINARY: 08, LAST ANNOTATION UPDATE)
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RA KATO H., OHASHI T., NAKAMURA N., NISHIMURA Y., WATAKI T., GUTSUKA H.,
 RA TSUTOMOTO H., HASEGAWA A.,
 RT "Molecular cloning of equine interleukin-1 alpha and beta cDNAs."
 RL VET. IMMUNOL. 1990;NOV-DEC; 42:221-231(1995).
 DR EMBL: D42146; G1197798;
 DR PROSITE: P500953; INTERLEUKIN-1;
 DR PFAM: PF00340; Interleukin-1;
 DR SEQUENCE: 279 AA; 98008 MW; 11440923 CRC32;
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01-NOV-1998 (TEMPREL 08, LAST ANNOTATION UPDATE)
 DE SIMILARITY TO A CHCH4-CLASS ZINC FINGER
 GN B0432.9
 OS CAENORHABDITIS ELEGANS
 OC PHARADITIA METACOMA NEMATODA, SEPTENTENTIA PHARADITIA PHARADITIA
 OC PHARADITIA METACOMA NEMATODA, SEPTENTENTIA PHARADITIA PHARADITIA
 RN 111
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2
 RX MEDLINE: 94150718
 RA WILSON R, AINSFORTH R, ANDERSON K, BAYNES C, BERKS M, BONFIELD J,
 RA FULTON T, GUNDEL M, HANLEY T, JENSEN J, JOHNSON A, OXLEY M,
 RA TAYLOR S, TERRY E, FAVELL A, FULTON L, SAPPNER A, GREEN P,
 RA KIRSTEN J, HILLER L, TIEF M, JOHNSON L, JONES M, KERSHAW J,
 RA KIRSTEN J, LASTER N, LATREILLE P, LIGHTNING J, LLOYD C,
 RA MONTAGNE P, MONTAGNE M, PARSINS J, PERCY C,
 RA PIERCE L, POOLPA A, SANDERS D, SHOWNKEEN R, SMALDON N, SMITH A,
 RA SONNHAMMER E, STADEN P, STURTON J, THIEPPE-MIES J, THOMAS K,
 RA VAUDIN M, VAUGHAN K, WATKINSON P, WATSON A, WEINSTOCK L,
 RA WILKINSON-SPOAT J, WOHLDMAN P,
 RI "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RI elegans." 368132-38(1994).
 RL NATURE 368:32-38(1994).
 RN 121
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2
 RA HENKHAUS J, WOHLDMAN P,
 RI SUBMITTED (JAN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN 131
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2
 RA WATKINSON P,
 RI SUBMITTED (FEB-1998) TO EMBL/GENBANK/DBJ DATA BANKS
 DR EMBL: 080836, 0107142,
 DR EMBL: 080836, 0107142,
 DR EMBL: 080836, 0107142,
 SO SOURCE: 111 AA, 19710 MW, 102398 CPG32.

Query Match 5.44 Score 76.5, DB 3, Length 425,
 Best Local Similarity 19.7%, Pred. No. 22,
 Matches 34, Conservative 29, Mismatches 41, Totals 77, Gaps 6

01-NOV-1998 (TEMPREL 08, LAST ANNOTATION UPDATE)
 DE SIMILARITY TO A CHCH4-CLASS ZINC FINGER
 GN B0432.9
 OS CAENORHABDITIS ELEGANS
 OC PHARADITIA METACOMA NEMATODA, SEPTENTENTIA PHARADITIA PHARADITIA
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 RA WILSON R, AINSFORTH R, ANDERSON K, BAYNES C, BERKS M, BONFIELD J,
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 RA TAYLOR S, TERRY E, FAVELL A, FULTON L, SAPPNER A, GREEN P,
 RA KIRSTEN J, HILLER L, TIEF M, JOHNSON L, JONES M, KERSHAW J,
 RA KIRSTEN J, LASTER N, LATREILLE P, LIGHTNING J, LLOYD C,
 RA MONTAGNE P, MONTAGNE M, PARSINS J, PERCY C,
 RA PIERCE L, POOLPA A, SANDERS D, SHOWNKEEN R, SMALDON N, SMITH A,
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 DR EMBL: 080836, 0107142,
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 RA FULTON T, GUNDEL M, HANLEY T, JENSEN J, JOHNSON A, OXLEY M,
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 RA VAUDIN M, VAUGHAN K, WATKINSON P, WATSON A, WEINSTOCK L,
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01-NOV-1998 (TEMPREL 08, LAST ANNOTATION UPDATE)
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 RX MEDLINE: 94150718
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 RA FULTON T, GUNDEL M, HANLEY T, JENSEN J, JOHNSON A, OXLEY M,
 RA TAYLOR S, TERRY E, FAVELL A, FULTON L, SAPPNER A, GREEN P,
 RA KIRSTEN J, HILLER L, TIEF M, JOHNSON L, JONES M, KERSHAW J,
 RA KIRSTEN J, LASTER N, LATREILLE P, LIGHTNING J, LLOYD C,
 RA MONTAGNE P, MONTAGNE M, PARSINS J, PERCY C,
 RA PIERCE L, POOLPA A, SANDERS D, SHOWNKEEN R, SMALDON N, SMITH A,
 RA SONNHAMMER E, STADEN P, STURTON J, THIEPPE-MIES J, THOMAS K,
 RA VAUDIN M, VAUGHAN K, WATKINSON P, WATSON A, WEINSTOCK L,
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 RA HENKHAUS J, WOHLDMAN P,
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 RP SEQUENCE FROM N.A.
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 DR EMBL: 080836, 0107142,
 DR EMBL: 080836, 0107142,
 SO SOURCE: 111 AA, 19710 MW, 102398 CPG32.

Query Match 5.44 Score 76.5, DB 3, Length 425,
 Best Local Similarity 19.7%, Pred. No. 22,
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01-NOV-1998 (TEMPREL 08, LAST ANNOTATION UPDATE)
 DE SIMILARITY TO A CHCH4-CLASS ZINC FINGER
 GN B0432.9
 OS CAENORHABDITIS ELEGANS
 OC PHARADITIA METACOMA NEMATODA, SEPTENTENTIA PHARADITIA PHARADITIA
 OC PHARADITIA METACOMA NEMATODA, SEPTENTENTIA PHARADITIA PHARADITIA
 RN 111
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 RC STRAIN-BRISTOL N2
 RX MEDLINE: 94150718
 RA WILSON R, AINSFORTH R, ANDERSON K, BAYNES C, BERKS M, BONFIELD J,
 RA FULTON T, GUNDEL M, HANLEY T, JENSEN J, JOHNSON A, OXLEY M,
 RA TAYLOR S, TERRY E, FAVELL A, FULTON L, SAPPNER A, GREEN P,
 RA KIRSTEN J, HILLER L, TIEF M, JOHNSON L, JONES M, KERSHAW J,
 RA KIRSTEN J, LASTER N, LATREILLE P, LIGHTNING J, LLOYD C,
 RA MONTAGNE P, MONTAGNE M, PARSINS J, PERCY C,
 RA PIERCE L, POOLPA A, SANDERS D, SHOWNKEEN R, SMALDON N, SMITH A,
 RA SONNHAMMER E, STADEN P, STURTON J, THIEPPE-MIES J, THOMAS K,
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 RA WILKINSON-SPOAT J, WOHLDMAN P,
 RI "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RI elegans." 368132-38(1994).
 RL NATURE 368:32-38(1994).
 RN 121
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2
 RA HENKHAUS J, WOHLDMAN P,
 RI SUBMITTED (JAN-1997) TO EMBL/GENBANK/DBJ DATA BANKS.
 RN 131
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2
 RA WATKINSON P,
 RI SUBMITTED (FEB-1998) TO EMBL/GENBANK/DBJ DATA BANKS
 DR EMBL: 080836, 0107142,
 DR EMBL: 080836, 0107142,
 DR EMBL: 080836, 0107142,
 SO SOURCE: 111 AA, 19710 MW, 102398 CPG32.

GenCore version 4.5
Copyright (c) 1993 - 1998 Compugen Ltd

OM protein : protein search using SW model

Run on: June 22, 1999 11:01:26 Search time: 83.17 Seconds

(without alignments)
104.143 Million cell updates/sec

Hit: US-09-030-061-7

Percent: 812

Sequence: 1 NGRHCTTAVININQVL KTEENKSVPLTNHQS 157

Scoring table: ELOSUM62

Searched: 18076 seqs, 55165189 residues

Database: SPREMBL.8:
1: sp_fungi:
2: sp_human:
3: sp_invertebrate:
4: sp_mammal:
5: sp_mhc:
6: sp_oranell:
7: sp_phase:
8: sp_plant:
9: sp_bacteria:
10: sp_ferment:
11: sp_virus:
12: sp_vertebrate:
13: sp_unclassified:
14: sp_archaea:

Prod. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Prod. NO.	Score	Match	Length	DB	ID	Description
1	739.5	91.1	194	10	088749	088749 ratius porv
2	508	82.7	132	2	075599	075599 homo sapien
3	87	10.6	167	12	073099	073099 gallus gall
4	80	9.9	1196	7	038197	038197 bacterioph
5	80	9.4	1194	9	045916	045916 clostridium
6	80	9.9	1196	9	053550	053550 clostridium
7	79.5	9.8	414	3	024832	024832 elmeria max
8	79.5	9.8	267	4	029082	029082 sus scrofa
9	79	9.7	506	9	084859	084859 chlamydia t
10	78.5	9.7	161	10	062161	062161 mus muscula
11	77	9.6	1146	9	081778	081778 borrelia bu
12	77	9.5	885	10	008759	008759 mus muscula
13	76.5	9.4	866	8	024295	024295 esum sativ
14	75.5	9.4	1146	9	068317	068317 vibrio chol
15	75.5	9.3	893	2	075283	075283 homo sapien
16	75.1	9.1	120	9	050494	050498 streptococ
17	74.5	9.2	631	9	073025	073025 synechocyst
18	74	9.1	4410	1	017019	017019 saccharomyc
19	74	9.1	622	2	014854	014859 homo sapien
20	74	9.1	1139	2	014084	014084 homo sapien
21	74	9.1	628	2	014421	014421 homo sapien
22	74	9.1	1139	2	015073	015073 homo sapien
23	74	9.1	1204	2	004119	004119 caenorhabdi
24	74	9.1	1204	2	022177	022177 caenorhabdi
25	74	9.1	659	3	051029	051029 borrelia bu
26	74	9.1	659	14	057721	057721 pyrococcus
27	73	9.0	711	1	005892	005892 saccharomyc
28	73	9.0	711	4	047612	047612 felis silve
29	72	9.0	1248	8	065589	065589 arabidopsis

ALIGNMENTS

Query Match	Score	Length	Length
088749	739.5	194	194
075599	508	132	132
073099	87	167	167
038197	80	1196	1196
045916	80	1194	1194
053550	80	1196	1196
024832	79.5	414	414
029082	79.5	267	267
084859	79	506	506
062161	78.5	161	161
081778	77	1146	1146
008759	77	885	885
024295	76.5	866	866
068317	75.5	1146	1146
075283	75.5	893	893
050498	75.1	120	120
073025	74.5	631	631
017019	74	4410	4410
014859	74	622	622
014084	74	1139	1139
014421	74	628	628
015073	74	1139	1139
004119	74	1204	1204
022177	74	1204	1204
051029	74	659	659
057721	74	659	659
005892	73	711	711
047612	73	711	711
065589	72	1248	1248

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D1 01-NOV-1996 (TREMREL, 01, LAST SEQUENCE UPDATE)
D2 01-NOV-1998 (TREMREL, 08, LAST ANNOTATION UPDATE)
DE ANTP-139
GN ANTP-139
US BACTERIOPHAGE 1C
OC VIRUSES
OC (1)
RN RN
PP SEQUENCE FROM N.A.
RC STRAIN-468:
RX MEDLINE, 9430193.
RA HAUSER D F., EKUND M M., BOUDET P., POPOFF M R.:
RT "Organization of the botulinum neurotoxin C1 gene and its associated
R1 non-toxic protein genes in Clostridium botulinum O 468."
R4 Mol. GEN. ENVI. 243:641-649(1994).
R5 EMBL, X73722, C51C174.
R6
R7
R8 SEQUENCE 1196 AA: 138725 MW: 646642Z CRC42:
SQ

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ID	PRELIMINARY:	PRF:	885 AA.
AC	008759: P97482:		
AI	01-JUN-1996 (TEMPREL_06_CREATED)		
DI	01-JUN-1998 (TEMPREL_06_LAST_SEQUENCE_UPDATE)		
ET	01-NOV-1998 (TEMPREL_08_LAST_ANNOTATION_UPDATE)		
DE	UNOBTAINED PROTEIN ASSOCIATED PROTEIN E6-AP (EC 3.2.2.7):		
GN	UBE3A:		
OS	MUS MUSCULUS (MOUSE):		
OC	EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: MAMMALIA: EUTHERIA: EUMETAZOA:		
SC	SCIENTIFICNAME1: MURIDAE: MURINAE: MUS:		
FN	(1)		
RP	SEQUENCE FROM N.A.		

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DN      11-JAN-1998 (TEMPLEBEL 05: LAST SEQUENCE UPDATE)
DT      01-JAN-1998 (TEMPLEBEL 05: LAST SEQUENCE UPDATE)
DT      01-NOV-1998 (TEMPLEBEL 08: LAST ANNOTATION UPDATE)
DE      LIPOXYGENASE.
GN      LOX1.PS.5.
OS      PISUM SATIVUM (GARDEN PEA).
OC      EUKARYOTA, VIRIDICLADIAE, CHLAROPIHYTA/EMNEFROPHYTA SPORO, EUTROPHYTA:
OC      HACHEOCHRYTA, EUPHYLLIPHYTES, SPERMATOPHYTA, MAGNOLIOPHYTA:
OC      EUDICOTYLOPHYNES, POSITAE, FABALES: FABACEAE, PAPILIONOIDEAE, PISUM.
RN      (1)
RP      SEQUENCE FROM N.A
PC      STRAIN=CV, BIRTE;
RA      FORSTER C.;
RL      SUBMITTED (NEW-1997) TO EMBL/GENBANK/EBI DATA BANKS.
DR      EMBL: Y15410; E1173602;
DR      PROSITE: PS00081; LIPOXYGENASE_2; 1
DR      PROSITE: PS00711; LIPOXYGENASE_1; 1.
DR      Pfam: PF00305; lipoxygenase; 1
SO      SEQUENCE 866 AA; 27748 MW; 0F70E935 CDS32.

Query Match          9.4%; Score 76.5; Db: d; Length 893;
Best Local Similarity 21.5%; Pred. No: 86;
Matches: 10; Conservative: 29; Mismatches: 46; Gaps: 71; Cops: 8

CY      1 NEEGLPTTAVINININQGVAV-EKQGVVFRTMTTIGSANSFPTPEITLYVRESVPA 59
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TB      419 NLGSL-----VEKAVNLSQGLFLEHAFIPYINLNENAAVAAPLLEFKENSTKPL 474
CY      60 AVILSV-----KSKN-----STL-----SKNNKISF----- 83
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
TB      475 ALESLHPHSGLVGNSLSSVILFSGQGVSTWLSKAVIVNSCHOLSLNINRAV 554
CY      9? -----LEMLP-----FENL-----KSLLEFQKVAIENNEE 113
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
TB      535 VPEHIAINHLVHPINLPLLPHPRLTININSLARALLNAGLIIETPTLPSSSVPM 594
CY      114 ESSLVE 119
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DB      595 SSAAYK 600

RESULT 14
C68317 PFTIMINARY. DFT. 1146 AA.
AC C68317;
DT 01-AUG-1998 (TEMPLEBEL 07: CREATED)
DT 01-AUG-1998 (TEMPLEBEL 07: LAST SEQUENCE UPDATE)
DT 01-NOV-1998 (TEMPLEBEL 08: LAST ANNOTATION UPDATE)
DE SENSOR KINASE.
GN VIES.
OS VIRIDICHOLEPAE
OC BACTERIA, PROTEOBACTERIA: GAMMA SUBDIVISION: VIBRIONACEAE: VIBRIO.
DN (1)

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RA MEDLINE 98032723
 PA IERF S H, ANGELOPHTO M J, MERALANOS J T, CAMILLI A:
 RT "Nucleotide sequence and spatiotemporal expression of the vibrio
 cholerae vlsAB genes during infection.";
 PT J BACTERIOLOGY 180:2290-2305(1998)
 DR EMBL AF031552; G3123890; -
 SI SEQUENCE 114 AA 126484 MW 136936 GPGG2;

Query Match 94% Score 76.6 TR 3 Length 1116;
 Post 100% Similarity 23.4% Ered No. 1.2e-07
 Matches 33; Conservative 25; Mismatches 50; Gaps 23; Gaps

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 MGS EVSNILZAGHFMASHLILQVAVATLAINFLIKKQLSELSNATVSSVLAHRTS 113

